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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 ~ 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on: US-10-047-825-3 1354 May 3, 2003, 09:25:51; Search time 2621 Seconds (without alignments) 15034.414 Million cell updates/sec

Title:
Perfect score:
Sequence: Word size : Searched: Scoring table: OLIGO_NUC Gapext 60.0 2054640 segs, 14551402878 residues 16

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters:

Database : Post-processing: Listing first 45 summaries GenEmbl:*
1: gb_ba:*

em_in:* em_hum:*

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ALIGNMENTS

AUTHORS TITLE	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	CCU12314	RESITE 1
Ross,A.H. Investigation of peroxidase genes and genetic transformation in	1 (bases 1 to 1335)	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Cenchrus ciliaris	Cenchrus ciliaris.		U12314.1 GI:520567	U12314	Cenchrus ciliaris clone PX7 peroxidase mRNA, complete cds.	CCU12314 1335 bp mRNA linear PLN 02-AUG-1994		

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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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160562 bp DNA linear HTG 02-AUG-2002 OFYZE SALIVE (japonica cultivar-group) chromosome 2 clone OSJNBA0082C09, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP005613
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Thesis (1994) Botany,
2 (bases 1 to 1335)
     Published Only in Database (2002)
2 (bases 1 to 160562)
Sasaki, T., Matsumoto, T. and Katayose, Y
                                                                         Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA, clone:OSJNBa0082C09
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SLGTLISLEGGRLSARDMLALSGAHRAQARCTTERGRI YGDTNIDASFAALQQOTCPR
SGGDGNLAPI DAQT PARFDNAYY TNLVSRRGLFHSDQELFNGGSQDALVRQY SSSPSQ
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/protein_id-"AAA20472.1"
/db_xref-"Gi:520568"
/translation-"MAAPTLMQCLLAISLLSFTAHAQLSTTFYASSCPNLQTVVRAAM
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/note=".expressed in leaves and is wound-induced"
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/cultivar="Bilo@la"
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Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

AL Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, MRL:http://rgp.dna.affrc.go.jp/, Tel:B1-298-38-7441, Fax:B1-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the finished sequence as soon as it is available and
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This is a 'working draft' sequence.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa.
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Submitted (01-AUG-2002) Takuji Sasaki, National Institute
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/chromosome="2"
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/33079 c 35854 g 45760 t
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                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.cseries: IRAL Plate: 21 Row: h Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yeast UBC4/5), clone MGC:14673 IMAGE:4106710, mRNA, complete cds...
                                                                                                                                                                                                                                                       passed the following selection identity to protein.
                                                                                                                                                                                                                                                                                                                                          Clone distribution:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
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Similarity 100.0%;
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/product="ubiquitin-conjugating enzyme to yeast UBC4/5)"
/protein_id="AAH05980.1"
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/clone="MgC:14673 IMAGE:4106710"
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/lab_host="DH10B"
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/chromosome="2"
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/cultivar="Nipponbare"
                                                                                   /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                           http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
4., Schmutz, J., Grimwood, J., Rodrique
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1322 CTTTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1354
9334 TTCAACGCCGGTCGCAGGACGCGCTGGTGAGG 9302
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NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the yieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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2 (bases 1 to 135792)
2 saski, T., Matsumoto, T. and Yamamoto, K. Direct Submission
Sibmitters ...
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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LLSICSILCDPNPDDPLVPDIAQIYKSDKEKYNRHAREWTQKYAM"
a 311 c 261 g 463 t
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30304 c 30206 g
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/chromosome="6"
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a valiable and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced
                                     1 (bases 1 to 950)
Weng, C.K. and To, K.Y.
                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
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Oryza sativa (japonica cultivar-group) chromosome 6 clone
OSJNBA0016D02, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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|cultivar="Nipponbare"
|/db_xref="taxon:39947"
|/chromosome="6"
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                      2 (bases 1 to 186896)
Tomlinson,C., Dixon,R., Kozlowicz,A. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-121A1
Unpublished (2001)
3 (bases 1 to 186896)
Waterston,R.H.
                                             Direct Submission
Submitted (19-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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AC019057.8 GI:15668119
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/proteth_id="AAK63358.1"
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/translation="MATVSSASAALRTISSSSKLSSAFQTKKIQSFKLPNPLISQNH
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/EC_number="5.3.99.6"
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/clone="TR3-F21"
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Data from ACO92170 and ACO64870 was used to finish this clone, ACO19057. Polymorphisms exist between RP11-121A1, RP11-814G20, and RP11-575E20. Location/Qualifiers 1. 186896 /organism="Homo sapiens" /db_xref="reaxon:9606" /chromosome="2" /clone="1b="RPCI-11" /clone="RP11-121A1" /clone=1ib="RPCI-11" /clone=1ib="RPCI-11" /clone=1ib="RPCI-11" /clone=1ib="RPCI-11" /clone=1ib="RPCI-11" /clone=1ib="RPCI-11" /rept_family="AT_rich" repeat_region	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis Sequence, see http://genome.wustl.edu/gsc SOURCE INFORMATION: The RCCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) WECTOR: pBACe3 6 NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the Jeft is RP11-814G20; the clone sequenced to the right is RP11-575E20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-12IA1; actual end is at base position and compact and c	AUTHORS Waterston, R. TITLE Direct Submission JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA COMMENT On Sep 19, 2001 this sequence version replaced gi:15144336. COMMENT Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: sapiensewatson.wustl.edu
/rpt_f /r	repeat_region 1397414708 repeat_region 140501423614259 repeat_region 1423614259 repeat_region 1423614259 repeat_region 1430914360 repeat_region 1430914360 /rpt_family="(CA)n" repeat_region 1430915042 /rpt_family="L1" repeat_region 1519115345 /rpt_family="L1" repeat_region 1519115347 repeat_region 1536815047 /rpt_family="L1" repeat_region 1544815500 /rpt_family="AT_rich" repeat_region 1544815507 repeat_region 1544815507 repeat_region 151416527 repeat_region 152916527 repeat_region 153916527 repeat_region 1539917978 repeat_region 1598917978 repeat_region 1758418078 repeat_region 1758418078 repeat_region 185418073 repeat_region 185418073	repeat_region 60756195 repeat_region 6776195 repeat_region 67276776 repeat_region 7327576 repeat_region /rpt_family="MIR" repeat_region /rpt_family="MIR" repeat_region 83618403 repeat_region 90259325 /rpt_family="Alu" misc_feature 900910233 /note="match to EST BG674364 (NID:gl3905760)" repeat_region 94979880 /rpt_family="MIR" repeat_region 97919886 /rpt_family="L2" repeat_region 131413229 /rpt_family="CT-righ"

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                                                                                            Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-63'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology construction, 5'-63'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 2.4%; Score 32; DB 9; L
1 Similarity 100.0%; Pred. No. 6.3e-06;
32; Conservative 0; Mismatches 0;
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Homo sapiens primary endothelial cells of human umbilical vein cDNA.
to mRNA, clone_lib:HUV clone:HUV00250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK026389 1253 bp mRNA linear PRI 29-SEP-2000 Homo sapiens cDNA: FLJ22736 fis, clone HUV00250, highly similar to AF131821 Homo sapiens clone 24877 mRNA sequence.
                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/rpt_family="(TTTTTG)n"
26161. .26212
/rnt fer...
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    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                             Location/Qualifiers
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29550. .29843
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29272. .29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequenced by Qiagen (Hilden/Germany) within the 2DNA sequencing consortium of the German Genome Project.
This clone (DKFZP686M0979) is available at the R2PD in Berlin. Please contact the R2PD: Ressourcenzentrum, Heubharwey 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.dc.Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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Homo sapiens mRNA; cDNA DKFZp686M0979 (from
AL833641 GI:21734288
                                                                                                                                                                                                                         31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duesterhoeft, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C. and
                                                                                                                                                                                                                                                                                                                                                                          /clone="DKFZp686M0979"
/tissue_type="cDNA-collection"
/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sf1; host
DH10B; sites Sf11A + Sf11B"
/dev_stage="adult"
1422. .1427
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veln"
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/db_xref="taxon:9606"
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/note="cloning vector pME18SFL3"
1844 bp
from Patent W00073348.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1844)
Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Tumas, D.,
Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of immune related
                                                                                                     1844 bp
Sequence 175 from Patent WO0208284.
AX454590
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AX088940 AX089940.1 GI:13443981
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1 (bases 1 to 1844)

Baker, K. P., Goddard, A., Gurney, A. L., Hebert, C., Henzel, W., Kabakoff, R. C., Shelton, D. L., Smith, V., Watanabe, C. K. and Wood, W. I. Methods and compositions for inhibiting neoplastic cell growth Methods and compositions for inhibiting neoplastic cell growth Patent: WO 0073348-A 23 07-DEC-2000;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
564 c 590 g 29:
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RESULT 15 AX491068 LOCUS DEFINITION ACCESSION VERSION	nes 324 787	Query Match Best Local	BASE COUNT ORIGIN	JOURNAL: FEATURES SOUTCE	AUTHORS TITLE	SOURCE ORGANISM	RESULT 14 AX464342 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy 1324 T Db 1787 T	Query Match Best Local Matches 3	BASE COUNT	FEATURES	JOURNAL	TITLE	REFERENCE AUTHORS
AX491068 1844 bp DNA linear PAT 16-AUG-2002 Sequence 175 from Patent WOO200690. AX491068 AX491068 AX491068 GI GI:22323871	VALIVE U; MISHACCHES U AAAAAAAAAAAAAAAAA 1354 	h 2.3%; Score 31; DB 6; Length 1844; Similarity 100.0%; Pred. No. 1.2e-05; Todols 0: Cana	/organism="Homo sapiens" /db_xref="taxon:9606" 398 a 564 c 590 g 292 t	07-JUN- iers	Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Goddwski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX464342 Sequence 475 from Patent WOO140466. AX464342 AX464342.1 GI:21899187	AAAAAAA 1354 AAAAAAAA 1817	ch 2.3%; Score 31; DB 6; Length 1844; 1 Similarity 100.0%; Pred. No. 1.2e-05; 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/i1044 /organism*Homo sapiens* /db_xref="taxon:9606" 398 a 564 c 590 g 292 t	Godowski, Paul J. (US); Gurney, Austin I h J. (US); Marsters, Scot A. (US); Pan, las F. (US); Stephan, Jean-Philippe F. n K. (US); Williams, P. Mickey (US); Wc in/Qualifiers	olving angiogenesis 08204-A 175 31-JAN-2002; 10. (US) ; Baker, Kevin P. (US) ; Ferrara, N . Hanspoter (US) : Govriteon Mary F. (US)	, Stephan, J.P., Watanabe, C.K., Williams, P.M., and methods for the diagnosis and treatment	p.T. Gurnev.A.T., Hillan.K.T., Marsters.S.A., Dan.T.

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KEYWORDS
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                                                                             Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis patent: WO 0200690-A 175 03-JAN-2002; Genentech, Inc. (US)
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seq length: 0
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Post-processing: Listing first 45 summaries

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hits satisfying chosen parameters:

Searched:

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Scoring table: Sequence:

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate can in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate can in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compoun (g) determining whether prostate cancer has metastasized in a patient) assessing the aggressiveness or indolence of prostate cancer in
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RESULT 3
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Best Local S
Matches 32
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient; (I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 7364; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate pharmacogenomic
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(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in
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(d) assessing the efficacy of a therapy
            The invention relates to an isola
a nucleotide sequence given in Ta
specification or its complement.
(a) assessing whether a patient i
                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usei for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV14239
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                                                                                                                               Claim
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                               2374; 11750pp;
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gene; ss.
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in Tables 1-9 (ABV00010-ABV62213)
ment. (I) is useful for:
lent is afflicted with prostate can
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                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for inhibiting prostate cancer
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                                                                 ) comprising of the
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RESULT 3
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proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammacory activities, and can be us in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                       AAC98773 to AAC99231 encode the human pancreatic
                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 531-532; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-579444/54.
P-PSDB; AAB54058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC98823;
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    is also useful as a pharmacodyanamic or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 16
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Pred. No.
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                                                                                                                                                                                                                                                                          cancer associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate
                                                                                                                                       and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especial, y cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AA099232 to AAC99240 and AAB54467 represent
                                                                                                                        Sequence 1527 BP; 397 A; 426 C; 394 G;
                                                                                                                                                                                  sequences
                                                                                                                                                                               used in the exemplification of the present invention.
2.4%; DU
100.0%; Pr
100.0%; Pr
                                                                                                                        308 T; 2 other;
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Дb 1487 1323 TTTTTCGGAAAAAAAAAAAAAAAAAAAAAA 1354

Query Match Best Local S Matches 32

l Similarity 32; Conserv

Conservative

Score 32; ; Pred. No.

DB 21; I . 0.0043; ches 0;

Length 1527; Indels

0;

0;

Mismatches

AAZ98108 standard; cDNA; 1722 ВP

09-MAY-2000

Human secreted protein encoding nucleotide sequence SEQ ID secreted protein; diagnosis; cytostatic; immunosuppressive; NO:102.

antiinflammatory; nootropic; neuroprofective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; respiratory disorder; reproductive disorder; gastrointestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative; ss.

Homo sapiens.

WO200004140-A1

27-JAN-2000

14-JUL-1999; 99WO-US15849

15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 98US-0092921. 98US-0092922. 98US-0092956.

(HUMA-) HUMAN GENOME SCI INC

Lafleur DW, Mucenski M, MS, Komatsoulis G, Duan , Ebner R, Olsen HS, , Endress GA, Soppet Soppet DR; RD, Rosen CA, MUDIE ; , Brewer LA, Florence Rosen CA, Moore PA, lorence KA, Shi Y; Young PE;

2000-161128/14. DB; AAY87155.

New isolated human ated human genes, useful for diagnosis and treatment neurological or blood disorders -

494pp; English

The polynucleotide sequences given in AAZ98017 to AAZ98108 encode the

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CC human secreted proteins given in AAY87064 to AAY87223. Human secreted CC protein can have activities based on the tissues and cells the genes are CC expressed in. Examples of activities include: cytostatic; Immunosuppressive; antiinflammatory; nootropic: neuroprotective; and CC immunosuppressive; antiinflammatory; nootropic: neuroprotective; and CC antiallergic. The polynuclectides and their corresponding secreted CC polypeptides are useful for preventing, treating or ameliorating medical CC conditions, e.g. by protein or gene therapy. Also pathological conditions CC can be diagnosed by determining the amount of the new polypeptides in a CC sample or by determining the presence of mutations in the new polynucleotides. Human secreted protein s and their polynucleotides can CC tumours, neurodegenerative disorders, diseases of the immune system, CC tumours, neurodegenerative disorders, diseases of the immune system, CC allergies, Alzheimer's diseases, behavioural disorders, schizophrenia, CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries, CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, CC disorders, respiratory disorders and metabolic disorders. The CC disorders, The proteins are also useful for identifying their CC preservatives. The proteins are also useful for identifying their the proteins or polynucleotides can also be used as food additives or the examplification of the noncent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psoriasis; sepsis; diabètes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder, Alzheimer's disease; food additive; anglogenic disorder; kidney disorder; pastrointestinal disorder; allergy pregnancy related disorder; endocrine disorder; infection; wound healing cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1722 BP;
WO200151504-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein-encoding gene 71 cDNA clone HDPOZ56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2001
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                                                                                                                                                                                    sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; proliferative disorder; cancer; tumour; asthma; abnormality; developmental abnormality; haematopoietic disorder:
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                                                                                                                        /*tag= b
122..1015
                                                                                                                                                                                                                                                                           /*tag= a
/product= "Human
/transl_except= (
                                                                                                                                                                                    59..121
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                            /product-
                                                                                                                                                                                                               /transl_except=
/transl_except=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%;
                                                            "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31;
Pred. No
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                                                                                                                                                                                                               n secreted protein precursor"
(pos:260..262, aa:Xaa)
(pos:401..403, aa:Xaa)
(pos:695..697, aa:Xaa)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergy;
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CC protein genes, and AREGO41-AREGO42 represent the proteins they encode.
CC protein genes, and AREGO41-AREGO43 represent the protein fragments.
AREGO613-AREGO42-AREGO43 represent the protein fragments.
CC The secreted proteins and their genes are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or yens therapy.
CC Pathological conditions can be diagnosed by determining the amount of the cent of the insured protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, concer, tumours, foetal and developmental abnormalities, diseases (e.g., rheumatoid arthritis), inflammation, altergies, congultive disorders (e.g., Alzheimer's disease, Parkinson's disease), cc ognitive disorders, schizophrenia, asthma, skin disorders (e.g., anglogenic disorders, schozorine disorders, and infections. The crophenis can also be used to ald wound healing and epithelial cell corpolations can also be used to ald wound healing and epithelial cell corpolation of the invention can be used in alleviating symptoms associated corpolation of the invention can be used in alleviating symptoms associated corpolation of the invention can be used in alleviating symptoms associated corpolation of the invention can be used in alleviating symptoms associated corpolation of the invention can be used in alleviating symptoms associated corpolation of the invention can be used in alleviating symptoms associated corpolations. The present sequence represents a human secreted protein-encoding cDNA of the disorders mentioned above, and in sagnostic immunoassays e.g., and can be used to manufact the condition of the corpolation of the corpolation of the corpolation of the corpolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 737-738; 864pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafleur DW,
Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001
                                             present sequence represents a human secreted protein-encoding cDNA of invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duan DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore PA,
Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shi Y;
Soppet DR;
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Sequence 1722 BP; 376 A; 534 C; 538 G; 269 T; Ų, other;

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οy
                                        Matches
                                                           Query Match
1655 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAAA 1685
                    1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAA 1354
                                                  Local
                                                  Similarity
                                         Conservative
                                                  100.0%;
                                                            2.38;
                                                           Score 31;
                                         0,
                                                  Pred
                                         Mismatches
                                                   .
No.
                                                 DB 22;
. 0.01;
                                         0
                                                           Length 1722;
                                          0
                                          Gaps
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0

В

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ABK69818
                                        RESULT
                                 ABK69818 standard;
                 (first entry)
                                 cdna;
                                 1722
                                 BP.
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ss; gene; secreted protein; gene therapy; immunosuppressive; tic; antirheumatic; antiproliferative; cytostatic; cardia cardiant;

Human secreted

protein gene

71

#2

Homo sapiens.

04-APR-2002 WO200226931-A2

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RESULT 8
AAA37046
ID AAA37046 standard; cDNA;
                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (or its of fragment, homologue complement or alleik variant) encoding a human or secreted protein (and its fragment, domain, epitope, variant, secreted comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell comprising the partner of the secreted protein and a method of identifying a binding that expresses the secreted protein and a method of identifying a binding that expresses, treat or ameliorate a medical condition in e.g. or revent, diagnose, treat or ameliorate a medical condition in e.g. or for example autoimmune diseases e.g. rehumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, verebrovascular disorders e.g. conneal infection. Many other diseases and fungi and collar disorders are listed in the specification. The polypeptides can also be used as a food additive or prevent of primary tissues, to regenerate tissues and in change changes and one apithelial cell proliferation. The prevent conservative to increase or decrease storage capabilities. The present expression to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                          Novel 71 isolated secreted polypeptides and polypucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2000; 2000US-234925P.
12-JAN-2001; 2001WO-US00911.
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Olsen H, Brewer LA, Florence KA,
Mucenski M, Ebner R;
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                          376 A;
                                                                                                                                                                                   2.3%;
      1843
                                                                                                                                                                                                                                            534 C; 538 G;
                                                                                                                                                                   0;
                                                                                                                                                                 Score 31; DB; Pred. No. 0.(
      ВP
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J.01;
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Young PE,
                                                                                                                                                                                                     Length 1722;
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Soppet DR;
                                                                                                                                                                   0;
      Human; PRO polypeptide; membrane bound protein; receptor; d'agnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO1265 (UNQ636) cDNA sequence SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1998;
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                                        9805-0100710
9805-0100919
9805-0100848
9805-0100849
9805-0101064
9805-0101071
9805-0101471
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Query Match Best Local Matches

Similarity

Sequence 1722 BP;

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30-SEP-1998

30-SEP-1998

30-SEP-1998

30-SEP-1998

01-CCT-1998

02-CCT-1998

07-CCT-1998

07-CCT-1998

07-CCT-1998

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21-CCT-1998

21-CC
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29-SEP-1998;
30-SEP-1998;
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9805-0103315.
9805-0103315.
9805-0103328.
9805-0103395.
9805-0103401.
9805-0103673.
9805-0103679.
9805-0103711.
9805-0104957.
9805-0104957.
9805-0104957.
                                                                                                                  98US-0105097.
98US-0105807.
98US-0105807.
98US-0106082.
98US-0106033.
98US-0106033.
98US-0106033.
98US-0106034.
98US-0106384.
98US-0106365.
98US-0106365.
98US-0106365.
98US-010639.
98US-010639.
98US-0106902.
98US-0106902.
98US-0106902.
98US-0106903.
98US-0106903.
98US-0106903.
98US-0106903.
98US-010893.
98US-0108803.
98US-0108803.
98US-0108803.
98US-0108803.
98US-0108803.
98US-0108853.
98US-0108853.
98US-0108853.
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98US-0108853.
98US-0108853.
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98US-0105104.
98US-0105169.
98US-0105266.
98US-0105693.
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98US-0103258
                                                                       INC
RESULT 9
AAX877
ID AAXX
XX
AC AAXX
XX
CDN 27-5
XX
CDN FFH Key
FFT CDS
FFT CDS
FFT Sig.
FFT mat.
FFT mat.
FFT Mat.
FFT T Sig.
FFT Sig.
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Best Local S
Matches 31
                                                                                                                                                                                                                      05-JAN-1998;
29-APR-1998;
22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37130 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1843 BP; 397 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 49; 773pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-237871/20.
P-PSDB; AAY99364.
                          WPI; 1999-430385/36.
P-PSDB; AAY06480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA clone encoding human PRO1265, amplified in tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09935170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO1265; UNQ636; cancer; tumour; diagnosis; therapy; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX87257
                                                                                                                       Botstein
                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                              20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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31; Conserv
                                                                                                  D, Goddard A, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA; 1844 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                      98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
98US-0088742.
98US-0107783.
                                                                                                                                                                                                                                                                                                                                                                                                99WO-US00106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= 79..141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
142..1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%;
                                                                                                                            Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
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Mismatches

DB 21; . 0.01;

Length 1843;

The

Indels

0,

Gaps

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מה של היה את היה של היה היה היה של היה ש

Baker ~

Goddard

P,

Gurney

ΑĽ,

Smith V,

Watanabe

CK,

Wood WI;

Hillan

Ğ,

Lawrence DA;

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This is the nucleotide sequence of cDNA clone DNA60764 (ATCC 203452) coding for human PRO1265 (UNG636) (see AAV66480). The clone was isolated from an adenoid tissue library. Amplification of DNA60764 on chromosome 19 occurs in various lung and colon tumours and cell lines, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed tot PRO1265 are expected to find use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX6477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferatio
     WPI; 2000-452188/39
P-PSDB; AAY93687.
                                                                                                                                                                                                                                                                                                                                                                                        WO200037640-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding novel polypeptide PR01265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA46906 standard; cDNA; 1844 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1844 BP; 398 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 7; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody against proteins expressed tumor diagnosis and treatment
                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.3%; So ilarity 100.0%; F Conservative 0;
                                                                      Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                         99WO-US28409.
99WO-US28301.
99WO-US28565.
                                                                                                                                                                                                              99WO-US05028.
99WO-US12252.
99WO-US20111.
99WO-US21090.
                                                                                                                                                                                             99WO-US28313
                                                                                                                                                                                                                                                                                                                     99WO-US30095
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 79..1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                      P
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                                                                      Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in neoplastic cells, useful for
                                                                      Hillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 1844; 0.01;
                                                                      <u>,</u>×
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                                                                      Lawrence DA,
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                                                                      Roy
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                                                                      MA;
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Best Local S
Matches 31
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
                                                                                                                                       06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                            20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO315, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1844 BP; 398 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 50; Fig 7; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                               09-DEC-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                                                                    02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                    01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000; 2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200140466-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA sequence encoding for PR01265 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS21481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
31; Conserv
                                                   2000WO-US04342.
2000WO-US04414.
2000WO-US04914.
2000WO-US05004.
2000WO-US05601.
                                                                                                                                       2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                              99WO-US28565.
99US-0170262.
99WO-US30095.
                                                                                                                                                                                                              99WO-US31243
                                                                                                                                                                                                                                                                                                                                                     99WO-US28634
                                                                                                                                                                                                                                                99WO-US30911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 31; DB
100.0%; Pred. No. 0.
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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RESULT 10 AAA46906 ID AAA46

03-OCT-2000 AAA46906; В

Query Match Best Local : Matches

0

29-JUN-2000.

16-DEC-1999;

30-NOV-1999; 30-NOV-1999; 01-DEC-1999;

02-DEC-1999;

Botstein D, Wood WI;

08-MAR-1999; 02-JUN-1999; 01-SEP-1999;

15-SEP-1999

gluten-sensitive enteropathy; skin disease; ermatitis; food hypersensitivity; urticaria; ersensitivity pneumonitis; graft rejection;

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ARESULT 12
AAD02920
ID AAD022
XX AAD02
XX 31-MA
XX 31-MA
XX Human
XX Human
KW antir
KW antir
KW antir
KW antid
KW antid
KW spord
KW spord
KW sarcc
KW demye
KW demye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bloattive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or cC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear utricular supporting cells or cC monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen
Smith V,
Human; PRO1265; antiinflammatory; dermatological; immunosuppressive; antitheumatic; antiarthritic; osteopathic; antianaemic; haemostatic; antithyroid; antidiabetic; antivarial; antipsoriatic; antiallergic; antiasthmatic; inhibitor; therapy; systemic lupus erythematosis; spondyloarthropathy; systemic sclerosis; systemic vasculitis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; autoimmune thrombocytopenis; immune-mediated renal disease; hepatitis; demyelinating polyneuropathy; Guillian-Barre syndrome; Whipple's disease; hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis;
                                                                                                                                                                                                                                                                                                                                                                                                                              1787
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other
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P-PSDB; AAU12409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker
                                                                                                                                                                                                                                                                                                                         AAD02920 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1844 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , funt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lated, secretory and transmembrane PRO polypeptide used to detect
er PRO polypeptides, link bioactive molecules to cells expressing
polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΚP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Fig 475; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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ME, Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000WO-US13705.
; 2000WO-US14042.
; 2000WO-US14941.
; 2000WO-US15264.
; 2000WO-US30873.
                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                                                                                                                       (DNA60764-1533).
                                                                                                                                                                                                                                                                                                                           CDNA; 1844 BP
                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%;
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A, Godowski PJ, Gurney i
Tumas D, Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 22;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1844;
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AL, Sherwood S;,
ood WI, Zhang Z;
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16-DEC-1999;
18-FEB-2000;
01-MAR-2000;
30-MAR-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease; gluten-sensitive enteropathy; allergic rhinitis; atopic dermatitis; food hypersensitivit eosinophilic pneumonia; hypersensitivity pneumonitis; graitiversens-host-disease; idiopathic pulmonary fibrosis; graft-versus-host-disease;
                                                                                                                                                                                                                                                                                                31-AUG-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                               08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                                                                                                                                                         Goddard
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                                                                                                                                                                                                 2001-226690/23.
DB; AAY72874.
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                                                                                                                                                                                                                   Godowski
Wood WI
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99WO-US20111.
99WO-US20182.
2000WO-US04342.
2000WO-US04342.
2000WO-US0439.
2000WO-US13705.
2000WO-US13705.
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142..1779
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79..141
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                                                                                                                                                                                                                         Gurney
                                                                                                                                                                                                                                                                                                                                                      "Mature human PRO1265 protein"
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The present sequence is a cDNA (DNA60764-1533 clone) encoding PR01265 CC protein. PRO protein, its agonist or antagonist or its antibody which care capable of enhancing or inhibiting the proliferation of T-lymphocytes CC or of increasing the infiltration of inflammatory cells into a tissue care useful in the diagnosis and treatment of immune-related diseases CC in mammals. The PRO protein is useful for treating systemic lupus CC erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic carthritis, spondyloarthropathy, systemic sclerosis, iddopathic carcidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, CC thyroiditis, diabetes mellitus, immune-mediated renal cisease, cellitus, diabetes mellitus, immune-mediated renal cisease, confectious or autoimmune chronic active hepathitis, primary CC disease, infectious or autoimmune chronic active hepathitis, primary CC disease, infectious or autoimmune chronic active hepathitis, primary CC disease, autoimmune or immune-mediated skin diseases such as bullous chronic disease, erythema multiforme and contact dermatitis, psoriasis, callergic disease, erythema multiforme and contact dermatitis, psoriasis, callergic disease, erythema multiforme and contact dermatitis, psoriasis, contact diseases of the lung cuch as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-cc sensitivity pneumoniats, transplantation associated diseases such as such as sociation or craft versus-host-disease. New PRO polypeptides for treating immune related and inflammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthm Claim 2; Fig 1; 118pp; English. autoimmune hemolytic anemia, and ritis, systemic vasculitis, asthma. diabetes mellitus -T-lymphocytes

TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1817

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Best Local :
                                 Matches
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01-SEP-1999;
29-OCT-1999;
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02-DEC-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                             The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                       Baker KP, Botstein
Gao W, Goddard A,
Pan J, Paoni NF, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1787 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1817
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            1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                           therapy
                                                                                                                                                                                                              Secreted and transmembrane useful as hybridization protherapy .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding protein of the invention #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-2001
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                                                                           Sequence 1844 BP;
                                                                                                                                                                                      Claim 2; Fig
                                                                                                                                                                                                                                                        WPI; 2001-071395/08
                                                                                                                                                                                                                                                                              Watanabe
                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                          Local
Similarity
                                                                                                                                                                                                                                                                              Paoni NF, Roy MA,
E CK, Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%;
Conservative
                                 Conservative
                                                                                                                                                                                      49; 787pp; English.
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2000WO-US00376
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99WO-US28313.
99WO-US28551.
99WO-US30095.
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                           2.3%; 5-
100.0%; Pr
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                                           Score 31;
Pred. No.
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Pred. No.
                                 Mismatches
                                                                           590 G;
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Ö
                                                                                                                                                                                                                     and nucleic acids designated PRO, chromosome and gene mapping and gene
                                                                           292 T; 0 other;
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                                          DB 22
0.01;
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                                 Indels
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Hillan KJ;
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The present sequence is one of twenty eight nucleic acids encoding PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to trea various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, gliai, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological disorders.

Twenty eight nucleic acids encoding PRO polypeptides for treating various tumors, e.g. breast cancer, and inflammatory, angiogenic and immunological disorders

which other

are useful

Baker KP, (Shelton DL,

Goddard A,

Gurney AL, Watanabe CK,

Hebert C, Wood WI;

Henzel

Σ

Kabakoff RC;

P-PSDB;

2001-016509/02. DB; AAB50962.

Claim 20; Fig 23; 188pp; English.

is one of twenty eight nucleic acids encoding PRO

to treat

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ARESULT 14
ARAC91546
ID AAC91
XX AAC91
XX AAC91
XX Human
XX Human
XX Human
XX Homo
XX 
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2000WO-US08439
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99US-0141037
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ABLUSTA 15
ABLUSTA 15
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XX ABLUSTA 19-JU
XX Human
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KW Antia
FR 28-JU
PR 25-JU
PR 25-JU
PR 27-JU
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Best Local S
Matches 31
                           25-JUL-2000

28-JUL-2000

28-JUL-2000

28-JUL-2000

17-AUG-2000

17-SEP-2000

24-AUG-2000

17-SEP-2000

18-SEP-2000

18-SEP-2000

10-NOV-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human anglogenesis related cDNA PRO1265 SEQ ID
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(GETH
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                           2001US-0854208
2001US-0856280
2001US-0866028
2001US-0866034
2001US-0806034
2001US-0870574
2001US-0870574
2001WO-US17443
2001WO-US17800
2001WO-US19692
2001WO-US00000
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                                                                                                                                                                                    ; 2001US-0808689.
; 2001US-0816744.
; 2001US-0828366.
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2001WO-US06520.
2001WO-US06666.
2001US-0802706.
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2001US-0767609
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Pred. No.
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. 0.01;
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Matches 31
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Godowski N
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(GERR/)
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(FERR/)
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DB; ABB95510.
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PAONI N F.
STEPHAN J F.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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FERRARA N.
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PJ, Gurney A
P, Watanabe
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ε CK,
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1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophhebitis lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or anglogenic disorders in a mammal -
ТТТТСGGAAAAAAAAAAAAAAAAAAAAAA 1817
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L, Hillan KJ, Marsters SA,
CK, Williams PM, Wood WI,
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Pred. No.
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Total number of hits satisfying chosen parameters:
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US-09-280-116-185
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US-09-351-248-1
US-09-466-994-1
US-09-430-240-1
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US-09-780-175-96
US-09-118-256-1
US-09-118-256-2
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SOFTWARE: FastSEQ for W1
SEQ ID NO 385
LENGTH: 2943
TYPE: DNA
ORGANIZM: Homo Sapiens
US-09-404-879A-385
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US-09-167-681-29
              NUMBER OF SEQ ID NOS: 52
SOFTMARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 7152
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                        Sequence 29, Application US/09167681A Patent No. 6265561
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Patent No. 6468546
                                                                                                                                 APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
TITLE OF INVENTION: SULPOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
                                                                                                       CURRENT APPLICATION NUMBER: US/09/167,681A CURRENT FILING DATE: 1998-10-07
    FEATURE:
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Sequence 5, Appli	Sequence 242, App	Sequence 25, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 25, Appl	Sequence 25, Appl	`	Sequence 30, Appl	Sequence 30, Appl	Sequence 3, Appli	Sequence 21, Appl	Sequence 57, Appl	Sequence 43, Appl				

ALIGNMENTS

Query Match 2.1%; Score 28; DB 4; Lost Local Similarity 100.0%; Pred. No. 0.0085; Matches 28; Conservative 0; Mismatches 0; APPLICANT: Mitcham, Jennifer L. APPLICANT: King, Gordon E. APPLICANT: Algate, Paul A. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121,462C2 CURRENT APPLICATION NUMBER: US/09/404,879A CURRENT FILING DATE: 1999-09-24 Application US/09404879A for Windows Version 3.0 Length 2843; 0; Gaps

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LENGTH: 78
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                          Patent No. 6238864
GENERAL INFORMATION:
                                       Sequence 1, Application US/09118256 Patent No. 6238864
                                                                                                                                                                          Matches
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Best Local :
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CURRENT FILING DATE: 2001-02-08
TITLE OF INVENTION: ANALYTE DETECTION ASSAY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                PPLICANT: YAN,
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NAME/KEY: CDS
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Pred. No.
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, OTHER INFORMATION: Description of Artificial Sequence: Adaptor US-09-118-256-1
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LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
SEQ ID NO 2
LENGTH: 56
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CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,164
EARLIER FILING DATE: 1997-07-18
NUMBER OF THE TOTAL TOT
                                                                                                                                     SOFTWARE: PatentIn Ver.
SEQ ID NO 185
LENGTH: 558
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CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,164
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                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-03-26
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ORGANISM: Artificial Sequence
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                                                                                                     TYPE: DNA
OTHER INFORMATION: ADAM family of metalloprotease
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; SEQ ID NO 4
; LENGTH: 654
; TYPE: DNA
; ORGANISM: human
US-09-265-630-4
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APPLICANT: LEVINE, BETH C
APPLICANT: LEVINE, BECLIN AND USES THEREOF
TITLE OF INVENTION: BECLIN AND USES THEREOF
FILE REFERENCE: 50902-D/JPW/EMW
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Best Local
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NAME/KEY: misc_feature
LOCATION: (1)..(558)
OTHER INFORMATION: n = a,
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                              APPLICATION NUMBER: US/08/618,911 FILING DATE: Concurrently herewith ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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TITLE OF INVENTION: ALTERA
TITLE OF INVENTION: SEEDS
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STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
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REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
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             Query Match
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NAME: SIMON, SOMA
REGISTRATION NUMBER: 37,444
REFERENCE/DOCKET NUMBER: 365-US
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
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MEDIUM TYPE: Floppy disk
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L Similarity 100.0%; Pred. No.
27; Conservative 0; Mismatc
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(515) TN NO: 3:
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2.0%; Score 27;
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                                                                                                                                                                                                                                                                                                                      US/08/618,911
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 DB 2;
. 0.025;
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0.025;
             Length 777;
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Best Local

l Similarity 100 27; Conservative

0;

Mismatches

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Gaps

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; NAME/KEY: CDS
; LOCATION: (71)...(808)
US-09-716-161A-10
                               RESULT 12
US-07-991-587A-6
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US-09-716-161A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; ORGANISM: Mus musculus US-09-245-041-10
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Sequence 6, Application US/07991587A Patent No. 5384249
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                SEQ ID NO 10
LENGTH: 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09716161A Patent No. 6355482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/716,161A CURRENT FILING DATE: 2000-11-07
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 4 BINDING PROTEIN EXPRESSIC
FILE REFERENCE: RTS-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: OF BODY WEIGHT DISORDERS FILE REFERENCE: 7853-136
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 131
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Moore, K.
APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                             1328 CGGAAAAAAAAAAAAAAAAAAAAAAAAAA 1354
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                                                                                              1080 СGGAAAAAAAAAAAAAAAAAAAAAAA 1106
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Local Similarity 100.0%;
nes 27; Conservative
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ilarity 100.0%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                         DB 4;
. 0.024;
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                                                                                                                                                                                        Length 1112;
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                                                                                                                                                                           RESULT 13
US-08-309-985-6
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                                                                                                                                           Sequence 6, Application US/08309985 Patent No. 5494790
                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                       1328 СGGAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,865
REFERENCE/FOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP-333661/1991
APPLICATION NUMBER: JP-091044/1992
FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                 APPLICANT:
                                                                APPLICANT:
                                                                               APPLICANT:
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   NUMBER OF SEQUENCES:
                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELLEFAX: ZZ
TELEFAX: ZZ 6262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UPFILING DATE: 19930526 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                   Local Similarity
les 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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277 Park Avenue
   Sekine, Susumu
Hanai, No. 5494790uo
Hasegawa, Mamoru
VENTION: '2 3 Sialyltransferase
EQUENCES: 7
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                                                                            Watanabe, Etsuyo
Nishi, Tatsunari
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                                                                                                             Sasaki, Katsutoshi
                                                                                                                                                                                                                                                                                                     Conservative
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; Pred. No.
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. 0.023;
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RESULT 14
US-09-211-930-12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2028
TYPE: DNA
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09211930 Patent No. 5962265
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                            CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                          APPLICANT: Tyrell E. NO. 5952255ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HOMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERINE/THREONIE KINASE
FILE REFERENCE: PHM.70296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 236262
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1328 CGGAAAAAAAAAAAAAAAAAAAAAAA 1354
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OPERATING SYSTEM: Dos 3.3
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE S. PERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
STREET: 277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
CELL LINE:
CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/991,587
FILING DATE: 16-12-1992
APPLICATION NUMBER: JP-333661/1991
APPLICATION NUMBER: JP-091044/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 20-SEE
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STATE: New York
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melanoma
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; ORGANISM: Mus musculus ... US-09-211-930-12
Search completed: May 3, 2003, 11:28:51 Job time : 72 secs
                                                                             В
                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Mus musculus US-09-340-993-12
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US-09-340-993-12
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                                                                                                                                              Query Match
Best Local Similarity
Matches 27; Conserva
                                                                                                                                                                                                                                                                            SEQ ID NO 12
LENGTH: 2028
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Tyrell E. No. 6034228ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHA. 70296.N1
CUIDELEM NOTICEMENT WINDELD. 15 (200.220.002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.0%; Sometime 100.0%; Best Local Similarity 100.0%; Matches 27; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930 EARLIER FILING DATE: 1997-12-19 & 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1975 СССАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВ 2001
                                                                                                             1328 СССАВАВАВАВАВАВАВАВАВАВАВАВАВ 1354
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                                                                           1975 CGGAAAAAAAAAAAAAAAAAAAAAAAAAA 2001
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                                                                                                                                                  Conservative
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Pred. No.
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475 App
11 B3 App11
83 App11
475 App

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Result
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Perfect score:
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: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB_Seq:*
: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB_Seq:*
: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB_Seq:*
: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB_Seq:*
: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB_Seq:*
: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB_Seq:*
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US-10-001-054-23
US-10-053-107-1
US-10-028-072-475
US-10-123-904-475
US-10-176-918-475
US-10-176-918-475
US-10-176-918-475
US-10-176-921-475
US-10-176-921-475
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US-10-143-114-475
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US-09-984-271-102
US-10-001-054-23
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                      Sequence: 102, 12 Sequence: 1, Apg. Sequence: 1, Apg. Sequence: 475, 12 Sequence: 47
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>e.51, Appl 23, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appl 14, Appl 
  Sequence 102, Application US/09984271

Publication No. US20030040088A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: 71 Human Secreted Protei

FILE REFERENCE: PZ030P1

CURRENT FILING DATE: 2001-10-29

CURRENT FILING DATE: 2001-10-29

CURRENT FILING DATE: 001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 1527
TYPE: DNA
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US-09-984-271-102
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US-09-925-297-51
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA105
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APPLICATION
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l Similarity 100.0%;
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71 Human Secreted Proteins
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US-10-121-050-4818-83
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US-10-141-755-475
US-10-143-132-475
US-10-123-145-1
US-10-123-236-475
US-10-123-236-475
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US-10-123-292-475
US-10-124-813-475
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US-10-124-925-475
US-10-124-925-475
US-10-121-043-475
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Pred. No.
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; OTHER INFORMATION: n equals a,t,g, or US-09-984-271-102
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Best Local Similarity
Matches 31; Conserv
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LENGTH: 1722
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NAME/KEY: SITE

LOCATION: (401)

OTHER INFORMATION: I

NAME/KEY: SITE

LOCATION: (695)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC ITLE OF INVENTION: CELL GROWTH
                                                                                                                                                                                                                                                                                                                                                                     PPLICANT:
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R OF SEQ ID NOS: 267
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APPLICATION NUMBER: 60/092,921
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APPLICATION NUMBER: PCT/US99/15849
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                            FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-04-24
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FILING DATE: 1998-03-30
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FILING
              APPLICATION NUMBER: 60/090691
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No. US20020192209A1
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milarity 100.0%;
Conservative 0
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FILING DATE: 1999-06-22
APPLICATION NUMBER: 60/141037
FILING DATE: 1999-06-23
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FILING DATE: 1999-01-20
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APPLICATION NUMBER: 60/209832
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APPLICATION NUMBER: PCT/US01/27099
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Hillan, Kenneth J
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; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo Sapien
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         PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
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CURRENT FILING DATE: 2001-12-19
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                                                                                                                              PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-08-26
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FILING DATE: 2001-06-29
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Watanabe, Colin
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US-10-123-904-475
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; Sequence 475, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
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FILING DATE: 1998-07-01
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Wood, William
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    See File Wrapper or Palm

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APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 FILING DATE: 1998-04-29 APPLICATION NUMBER:

1998-05-07

60/084600 60/083545 60/083322 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999

APPLICATION NUMBER:

60/081817

FILING DATE: 1998-04-APPLICATION NUMBER: 60/081695

FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081203

FILING DATE: 1998-04-28 APPLICATION NUMBER:

FILING DATE: 1998-04-24

FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/

APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: 60/079663

FILING DATE:

1998-02-27

FILING DATE: 1998-03-25 APPLICATION NUMBER:

DATE: 1998-03-12

1998-03-20

60/078910 60/079294

FILING DATE:

1998-03-3

60/080165

APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-12

FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085579

APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 FILING DATE: 1998-05-1

APPLICATION NUMBER: 60/086414

FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/

60/085338 60/085323

APPLICATION NUMBER:

APPLICATION NUMBER: 60/090349
APPLICATION NUMBER: 60/090349

APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947

FILING DATE: 1998-06-

APPLICATION NUMBER: 60/089599

FILING DATE: 19/98-06-11 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17

APPLICATION NUMBER:

FILING DATE: APPLICATION NUMBER:

1998-06-10

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FILING DATE:

1998-06-10

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60/088026 60/087106 60/086430

FILING DATE: 1998-05-28 APPLICATION NUMBER: FILING DATE: 1998-05-22 APPLICATION NUMBER: FILING DATE: 1998-05-

APPLICATION NUMBER:

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US-10-140-470-475
US-10-140-475, Application US/10140470
; Sequence 475, Application US/10140470
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LENGTH: 1844
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ORGANISM: Homo Sapien
;-10-140-470-475
                                                               SEQ ID NO 47
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CURRENT FILING DATE: 2002-04-16
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NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
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                                 TYPE: DNA
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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US-10-175-746-475
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US-10-176-918-475
Sequence 475, Application US/10176918
Publication No. US20030027275A1
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Best Local Similarity
Matches 31; Conserv
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-19
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Wood, William
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                                                        Godowski, Paul J. Gurney, Austin L.
                                                                                   Gerritsen, Mary E. Goddard, Audrey
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Filvaroff, Ellen
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D. US20030027270A1
Tumas,Daniel
             Stewart, Timothy A.
                           Smith, Victoria
                                           Sherwood, Steven
                                                                                                                Gao, Wei-Qiang
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RESULT 11
US-10-176-921-475
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RESULT 12
US-10-137-865-475
: Sequence 475, Application US/10137865
: Publication No. US20030032155A1
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                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-921-475
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                                                                                                                                                                                                                                                                                  Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 475 LENGTH: 1844
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SEQ ID NO 475
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
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                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
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                                                                                                  1324 ТТТТСССАААЛААААААААААААААААААА 1354
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il Similarity 100.0%;
31; Conservative (
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31; Conservative
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Wood,William
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Gurney, Austin L.
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Filvaroff, Ellen
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o. 2.7e-06;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
TYPE: DNA
                           Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
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Best Local Similarity
Matches 31; Conserva
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APPLICANT
                                                                                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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CURRENT FILING DATE: 2002-05-03
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
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ORGANISM: Homo Sapier
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Wood,William
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Gurney, Austin L.
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Pred. No.
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US-10-140-474-475

DB 9; Lo

Length 1844;

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Prior Application removed - Se
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
TYPE: DNA
ORGANISM: Homo Saplen
US-10-142-431-475
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US-10-143-114-475
; Sequence 475, App
; Publication No. 1
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US-10-142-431-475
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Matches 31; Conserva
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                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauro
APPLICANT: DeForge, Laura
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                Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                 Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                       Beresini, Maureen
DeForge, Laura
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Filvaroff, Ellen
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Sherwood,Steven
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5. US20030036179A1
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::llarity 100.0%; Pred. No.
Conservative 0; Mismatc
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; SEQ ID NO 475
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-143-114-475
Search completed: May 3, 2003, 12:17:40 Job time: 149 secs
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                                                                                                               Query Match
Best Local Similarity 100.
Matches 31; Conservative
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APPLICANT:
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CURRENT FILING DATE: 2002-05-09
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Wood, William
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

ALIGNMENTS

AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CCU12314	RESULT 1
Ross, A	1 (ba	clade;	Sperma	Eukary	Cenchr	Cenchr	•	U12314	U12314	Cenchr	CCU123		

Pred. No.

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the number of results predicted by chance to have a

TITLE

Investigation of peroxidase genes and genetic transformation in

CCU12314
1335 bp mRNA linear PLN 02-AUG-1994
Cenchrus ciliaris clone PX7 peroxidase mRNA, complete cds.
U12314
U12314.1 GI:520567
Cenchrus ciliaris.
Cenchrus ciliaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Paniceae; Cenchrus.
1 (bases 1 to 1335)
Ross,A.H.

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                           ACCATCGTGCCCCTCGCCGCGCGACCGGGACCGAATCTTCTCGGCGGGCCGACCTGGAAC
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Thesis
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Direct Submission
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SUGTLISLEGGGRLSARDMIALSGAHHAQARCTTFRGRIYGDTNIDASFAALQQOTCPR
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/EC_number="1.11.1.7"
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/codon_start=1
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/clone_lib="lambda gt-10"
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/cultivar="Biloela"
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Location/Qualifiers
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160562 bp DNA
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OSJNBA0082C09, *** SEQUENCING IN PROGRESS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
                                        Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                    Direct Submission Submitted (01-AUG-2002) Takuji Sasaki, National Institute
                                                                                                                             Published Only in Database (2002)
2 (bases 1 to 160562)
Sasaki, T., Matsumoto, T. and Katayose, Y
                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Katayose,Y. oryza sativa nipponbare(GA3) genomic DN clone:OSJNBa0082C09
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CCGCCGCCGCGCGCCGCCGCGCCCGGCTCCGGCGACTCCAGCCTGGCGCGCCTCGA 98628
                  GCGGCAGCAGACGTGCC-----CGCGGTCCGGCGGCGACGGCAACCTGGCGCCCATCGA 761
                                                    CGCCAACTTCCGCGACCGCGTCTACAACGACACCAACATCGACCCGGCGTTCGCCGCGCT
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* This sequence will be replaced
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Location/Qualifiers
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Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Direct Submission
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3 (bases 1 to 1330)
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aavnseprmgasllrlhifhdcevqgcdasvllsgnegdappnkdslrgygvidsikga
ieavcngtvscadlityaardsvyalgsptmyvplgrnstgasaalaisplepetas
iqelvdafakkglsvtdmvalsgahtigqaqcstfrgriynetnidsafatqrqancp
                                                                                                                     RTSGDMNLAPLDTTTANAFDNAYYTNLLSNKGLLHSDQVLFNNGSTDNTVRNFASNAA
                                                                                                                                                                                                                                                                                                                                                                                                                         /product="peroxidase poc1"
/protein_id="AAF65464.2"
/db_xref="GI:8901180"
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/cultivar="IRBB10"
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KS 66506, USA
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Query Match

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                                                             CCAACCAAAACTCTGTTAGAGGGTTCGACATAATAGACACGATCAAGACCAGAGTTGAGG
                                                                                                                                                                                                                                                                                       CCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTG 217
                                                                                            CGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGG
                                                                                                                             GTGATGGGTCGCTACTGTTGGACGATACTGCCACTTTCACTGGCGAGAAGAACGCAGGAC
                                                                                                                                                            GCGACGGATCGATCCTTCTCGACG------CCGGAGGGGAGAGACACCCCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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/product="peroxidase flxper4"
/product="peroxidase flxper4"
/prodein_id="AAC05277.1"
/db_xref="g1:2944417"
/translation="famsLlassgsaqLaaneyarscptiltivrnamtqavnsenrm
/translation="famsLlassgsaqLaaneyarscptiltoTiktykveaa
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TNLFTMKGLTAADVTILSGAHTIGQARCTTFRQRIVNDTNIDPAFATTRRGNCPQAGA
GANLAPLDGTFTQETMRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAATFATD
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/dev_stage="21 day"
<1 1176</pre>
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/cultivar="Stormont Cirrus"
/db_xref="taxon:4006"
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Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
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OJ1077_A12, *** SEQUENCING IN PROGRESS
AP003991
AP003991.1 GI:15076799
HTG: HTGS-PHASE2.
                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, clone:OJ1077_A12
                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OJ1077_A12.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                 Published Only in Database (2001) 2 (bases 1 to 149417)
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ACCAGGAGCTGTTCGCCGCCGGCGGCGGCGGCAGGTCGTCGTCGCAGGACCCGCTGGTGC
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                                                                                    ACGTGTTCGACAACGGCTACTTCCGCGAGCTGACGAAGCAGCGCGGGCTGCTGCACTCGG
                                                                                                                                                                        TGTGCCCCGCGGCACCGGCGACGGCAACCTCGCGCCGCTGGACGCCGAGACGCCCG
                                                                                                                                                                                                                                                                                                                                                                                      ACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCG
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615; Conserv
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
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33053 c 33283 g
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Pred. No. 1.5e
0; Mismatches
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1.5e-43;
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TITLE
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VERSION
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SOURCE
ORGANISM
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                                     CTGCTGGTGGCTGCAGCTATGGCGTCAGTGGCATCGGCGCAGCTCTCGGCGACGTTCTAT 1,7
                                                               CTGGTCGCCGTTTCCCTCTCTCTGTGTCGCCCACGCACAGCTCTCGCCCCACGTTCTAT 153
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Oryza sativa.
Oryza sativa
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O.sat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reimmann,C.
Direct Submission
Submitted (07-JUN-1992) C. Reimmann, Institute for Plant Biology,
University of Zuerich, Zollikerstrasse 107, CH-8008 Zuerich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 1287)
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2 (bases 1
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X66125
                                                                                                                                                            321
                                                                                                                                                                                                                                 /product="peroxidase"
/protein_id="Can46916.1"
/protein_id="Can46916.1"
/db_xref="G1:20286"
/db_xref="G1:20286"
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PSSSLAELIGNFSRKGLDATDMVALSGAHTIGQAQCQNERDRIYNETNIDSAFATQRQ
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/EC_number="1.11.1.7"
377 c 353 g
                                                                                                                                                                                                                         FASNAAAFSSAFTTAMVKMGNISPLTGTQGQIRLSCSKVNS"
                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="pPIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa/cultivar="Nohrin"
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                                                                                                      Score 363.4; DB 8 Pred. No. 3.7e-43;
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TGCTCCAAGGTGAACTCCTAATTAAGGAGTA 985
                TGCCGGGTCGTCAACAGCTAGATACGACGCA 1018
                                                         ATGGTGAAGATGGGGAACATCTCGCCGCTGACCGGGACGCAGGGGGCAGATCAGGCTCAGC
                                                                             ATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGATCAGGCGCAAC
                                                                                                                                        GCGCTGGTGAGGCAGTACAGCGCCCAGCGCCTCGCTCTTCAACGCCGACTTCGTGGCAGCC
                                                                                                                                                                                   CTGTCCAACAAGGGGCTCCTGCACTCCGACCAGGTGCTCTTCAACGGCGGCAGCGCGAC
                                                                                                                                                                                                 CTGTCGCGGCGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGAC
                                                                                                                                                                                                                                              CTGGCGCCCGTGGACACGACGCCCAACGCCTTCGACAACGCCTACTACAGCAACCTG
                                                                                                                                                                                                                                                               CTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTCACCAACCTG
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RESULT 8
AF014467
LOCUS
DEFINITION
ACCESSION SOURCE KEYWORDS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales, Poales Phrhartoideae; Oryzae; Oryza.

1 (bases 1 to 1306)
Chittoor,J.M., Leach,J.E. and White,F.F. AF014467 Oryza sativa peroxidase AF014467 Oryza sativa. Oryza sativa defense response gene; bacterial blight. AF014467.1 GI:2429285 1306 bp mRNA linear F (POX22.3) mRNA, complete cds. PLN Tracheophyta; 27-SEP-1997

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                                                                                                             AACCAGACCGTCTCCTGCGCGACATCCTCGCCGTCGCCGCCCGTGACTCCGTCGTCGCG
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                TCGCTCGCCAACAGCAACCCCCCCGCCCCCGACGGCCAGCCTCGGCACGCTCATCTCCCTG
                                                 CTGGGAGGGCCATCATGGACGGTTCTGTTGGGGAGAAGGGACTCCACCACTGCAAGCGAG
                                                                                                                                                                            GGGTCGCTGAGGGGATTCAGCGTCATCGACAACGCCAAGGCGCGGGTGGAGGCCATCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-JUL-1997) Plant Throckmorton Hall, Manhattan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chittoor, J.M., Lea
Direct Submission
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/protesin_id="AAC49818.1"
/protesin_id="AAC49818.1"
/db_xref="GI:2429286"
/translation="MASATNSSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIK
/translation="MASATNSSLSLMLLVAAAMASVALSQDEQNAGPNVGSLRGFSVIDN
AKARVEAICNOTVSCADILAVAARDSVVALGGPSWTVLLGRRDSTTASDALARTDLPA
PSSSLAELIGNESRKGLDATDWALSGAHTIGQAQCONFRDRIYNETNIDAFATQRQ
ANCPRPFGSGDSNLAALDTTTPWAFDNAYYSNLLSNKGLLHSDQVLFNGGSADNTVRN
FASNAAAFSSAFTTAMVKMGNISPLTGTQGQIRLSCSKVNS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/strain="IRBB10"
/db_xref="taxon:4530"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="pathogen inducible"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="POX22.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="R2576S; L831"
/tlssue_type="leaf"
/note="mRNA isolated from rice leaves 12
infiltration with incompatible strain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="POX22.3"
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Submitted (15-JUL-1994) Annette H. Ross,
Botany, St. Lucia, Brisbane, Queensland,
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoldeae; Paniceae; Cenchrus.
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Cenchrus ciliaris clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cenchrus
                                                                                                                                                                                                                                                                                                                                                                   Investigation of peroxidase genes and genetic transformation
                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1255)
                                                                                             65. .1006
/EC_number="1.11.1.7"
                                                                                                                                         /organism="Cenchrus ciliaris"
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|/db_xref="taxon:35872"
|/tissue_type="wounded and unw
|/clone_lib="lambda gt-10"
             /product="peroxidase"
/protein_id="AAA20473.1"
/db_xref="GI:520570"
                                                              /codon_start=1
                                                                                 /note="expressed
                                                                                                                                                                                                                                       Location/Qualifiers
   translation="MASSVSGLLLMLCMAAVASAQLSATFYDTSCPNALSTIKSAVTA"
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                                      AGCAGACGTGCCCGGGGTC-----CGGCGGCGACGGCAACCTTGGCGCCCCATCGACGTGC
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                                                                                                                                                                                                                           CGCCGCGCGACATGACGGCGCTGTCGGGCGCGCGCACACCATCGGGCAGGCCCCGGTGCACCA 652
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TCCACTCGGACCAGGACCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTGAGGCAGTACA 886
                                                                                           AGGCCAACTGCCCCCGGCCCACCGGCAGCGGCGACGGCAACCTGGCGTCGACTCGACACGT
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PRPTGSGDGNLASLDTSTPYTFDNAYFKNLLSQKGLLHSDQELFNGGSTDNTVRNFAS
NPSAFSSAFAAANVKMASLSPLTGSQGQIRLTCSKAN"
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VEAICKQTVSCADILAVGARHSVVALGGPSWTVPLGRRDSTSGSAALANSDLPASRSF
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Oryza sativa L. (strain Nipponbare, sub_species japonica) root cDNA to mRNA, clone R2576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-JUN-1993) Yuzo Minobe, National Institute Agrobiological Resources, Rice Genome Research Program; 2-1-2, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice Genome Res. Program
National Institute of
Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:MINOBE@rtcs0.riken.go.jp, Tel:0298-38-7441, Fax:0298-38-7468)
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Minobe, Y.
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Peroxidase from rice
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Ehrhartoideae; Oryzeae; Oryza
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               Similarity
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0298-38-7468.
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                                                                               SSLAELIGNESKGLDVEDMVALSGAHFIGOAOCONERDRLYNEENIDSSEATALKAN
CPRPEGSGBSNLAELDTTFPNAEDSAYYNLLSNKGLLHSDQVLENGGSTDNTVRNES
SNTAAFNSAETAANVKNGNISPLTGTOGOIRLNCSKVN"
401 c 354 g 258 t
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/EC_number="1.11.1.7"
                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                      /tissue_type="root"
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                                                                                                                          CCCAGGGCAGATCAGGCTCAACTGCTCCAAGGTTAAC 1022
                                                                                                                                          CCGCCGGACAGATCAGGCGCAACTGCCGGGTCGTCAAC 1002
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                                  AP003544 135792 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 6 *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP003544.1 GI:13810550
HTG; HTGS_PHASE2.
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NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
GTGAGGCAGTACAGCGCCCAGCGCCTCGCTCTTCAACGCCGACTTCGTGGCAGCCATGATT 933
                                                                              CCCATCGACGTGCAGACGCCGGTGAGGTTCGACCACCCGACCTTCACCAACCTGCTGCTGCT
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Published Only in Database (2001)
2 (bases 1 to 135792)
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Direct Submission
Submitted (25-APR-2001) Takuji Sasaki, National Institute of
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/cultivar-"Nipponbare"
/db_xref-"taxon:39947"
/chromosome-"6"
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Librate Submission

Librate Submission

Librate (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasski@nias.affrc.go.jp, URR:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Pax:81-298-38-7468)

NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the finished sequence as soon as it is available and

* the accession number will be preserved.
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                    TCGCTCGCCAACAGCAACCCCCCCGCCCCCGACGGCCAGCCTCGGCACGCTCATCTCCCTG
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
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/chromosome="6"
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Mismatches 123;
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa peroxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77527
                                                                                                                                                                                                        /organism="Oryza sativa"
/strain="IRBB10"
/db_xref="taxon:4530"
/chromosome="7"
/note="pathogen and wound
/codon_start=1
/product="peroxidase"
/protein_id="AAC49819.1"
                                                                                                                            oryzae
                                                                                 /gene="POX8.1"
43. .990
                                                               /gene="POX8.1"
                                                                                                                                                                          /map="R2576S; L831"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                         Locati
                                                                                                                                                                                                                                                                                       lon/Qualifiers
                                                                                                                          pv. oryzae"
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814 CGGCGGGGCCTGTTCCACTCGGACCAGGACCTCTTCAACGGCGGGTCGCAGGACGCGCTG 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTTCGCGTCGCTCCGGCAGACAGACGTGCCCGCGCTCCGGCGACGCCAACCTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATGGGCAACCTGCTGCCGTCCTCCGGCACCGCCACGGAGGTCAGGCTCAACTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATGGGCAACGTTGGGGTGCTCACCGGCACCGGCCGGACAGATCAGGCGCAACTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCGCGGCCTGCTCCACTCCGACCAGGAGCTCTTCAATGGCGGCTCGCAGGACGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTTCGACGTGCAGACGCCCGACGCCTTCGACAACGCCTACTACCAGAACCTCGTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTTCGCGGCGCTGCGGAGCAGACGTGCCCGCGGTCCGGCGACGGCAACCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                   Chittoor, J.M., Leach, J.E. and manue.

Direct Submission
Submitted (18-0UL-1997) Plant Pathology, Kansas
Submitted (18-0UL-1997) Ranhattan, KS 66506, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chittoor, J.M., Leach, J.E. and White, F.F.
Differential Induction of a peroxidase gene family during of the by Xanthomonas oryzae pv. oryzae mol. Plant Microbe Interact. 10 (7), 861-871 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 defense response gene; bacterial blight
                                                                                                                                                             /note="mRNA isolated from rice leaves 12 hours following infiltration with incompatible strain of Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1220 bp mRNA linea (POX8.1) mRNA, complete
inducible"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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ORIGIN
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Best Local S
Matches 559
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                                                    156 GTCCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAG
   65
                                                                                                                                                                  96 GGTCGCCGTTTCCCTCCTCTCTGTGTCGCCCACGCACAGCTCTCGCCCACGTTCTATGC 155
                                                                                                              5
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                                                                                                              GGTCGACGTTACGATAAGCTGTATACGAATTCCGGCGCAGTTGTCGCCGACGTTCTACGA 64
                                                                                                                                                                                                                         al Similarity 61.6 559; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare partial mRNA for peroxiuase (pray year, AJ276227
AJ27627
AJ276227
AJ27627
AJ2762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 930)
Green,R.M. and Bevan,M.
Isolation and characterisation
powdery mildew infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JUL-2000) M. Bevan, 7UH, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1991) University of Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 930)
                                                                                                                                                                                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .914
/genr
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="pi
43. .911
                                                                                                                                                                                                                                                                                                                                                                   /gene="prx8"
/product="peroxidase"
a 308 c 262 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="peroxidase"
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/product="peroxidase"
/product="peroxidase"
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/protein_id="cAB99487.1"
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ANLDTTANTEDNAYYTTIAMSRRGILHBDQVLFNNDTTDNTVRNFASNPAAFSSAFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIKMGNIAPKTGTQGQIRISCSRVNS" <1. .42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="prx8"
/function="defence against plant pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /country="United Kingdom"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="d8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare
/cultivar="Midas"
                                                                                                                                                                                                                                                    25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ="prx8"
                                                                                                                                                                                                                            ;0
                                                                                                                                                                                                                      Score 339; DB 8;
Pred. No. 1.3e-39;
0; Mismatches 345
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CGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCGGCCGCCATCTACGGCGACACCCG

CGCACACGATCGGGCAGGCGCAGTGCACCTACCTCAGGGGAAGGATCTACAACGAGACCA 661

TCATCTCCCTGTTCGGCAGGCAGGGCCTGTCGCCGCGCGACATGACGGCGCTGTCGGGCG CGGCGAGCATGGACAGCGCTAACAACGACCTGCCTCCTTTCTTCGACCTCGAGAACC

622

601

682

TCATCAAGGCGTTCGGCGACAAGGGTTTCAGTGTCACCGACATGGTTGCTCTCAGGTG

GCGACGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACT ACATCGACGCCGGCTACGCGCGCGTCGCTCAGGGCCCAACTGCCCGCCGACGGCCGCACCG

796

721

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GCGACAGCAACCTGGCGGCGCTGGACACGACGCCCTACTCCTTTGACACCGCCTACT

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> 857 782 797 722 737

> > TCACCAACCTGCTGTCGCGGCGGGGCCTGTTCCACCTCGGACCAGGAGCTCTTCAACGGCG

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TCTCGTCGGCCATGGTGAAGATGGCCAACCTCGGACCACTCATCGGGAGCCAGGGACAGA TCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGA 976

961

ACAGCACGACAACACGGTCAGGAACTTCGCCTCCAACAGGGCGGCGTTCAGCAGCGCCT GGTCGCAGGACGCGCTGGTGAGGCAGTACAGCGCCCAGCGCCTCGCTCTTCAACGCCGACT ACAGCAACCTGCTGTCCAACAAGGGGCTCCTGCACTCCGACCAGGTGCTCTTCAACGGCA

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TTCCTAACAAGAATTCTCTCAGAGGCTTCAACGTCGTCGACAGCATCAAGACGCAGCATCG GGCCGAACCTGAACTCGGTGCGCCGGCTTTGAGGTCATCGACACCATCAAGCGGGAACCTTC

382

301 322 241

442 361 GGTGCGATGCGTACTGCTGGCGGACACGGCCACGTTCACCGGCGAGCAGAATGCTC GCTGCGACGGATCGATCCTTCTCGACG------CCGGAGGGGGAGAAGACCGCCG

AGGGCATCTGCAGCCAGACCGTCTCCTGCGCCGACATCCTCGCCGTCGCCGCCGCGACT 421

CCGTCGTCGCACTGGGAGGGCCGTCATGGACGGTTGGTCTCGGGAGGAGGGACTCAACCA

CGGCCAGCGCTCGCCAACAGCAACCCCCCCCCCCGACGGCCAGCCTCGGCACGC

562

481

541

Вр Ş

TGGTCGCCGTTTCCCTCCTCTCTCTGTGTCGCCCACGCACAGCTCTCGCCCCACGTTCTATG 154

155 62 95

274

ACACGTCGTGCCCCAGGGCGCTGGCCACCATCAAGAGCGCCGTGACGGCCGCCGTGAACA 181 CGTCCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGGCGGTGACCCAGGCCGTCGCAA 214 TGGCCGTGCTCCTGTGCCTCGCCGCCGCCGCCGCGGCGCAGCTGTCGCCGACGTTCTACG, 121 BASE COUNT ORIGIN

285

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/db_xref="G1:2429288"
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FFDLENLIKAFGDKGFSYTDMVALSGAHTIGOAOCTNFRGRIYNETNIDAGYAASLRA
NCPPTAGTGDSNLAALDTTTPYSFDTAYYSULLSNKGLLHDQVLFNGNSTDNTVRNF
ASKRAAFSSAFVSAMVKKANLGFLIGSQGQIRLSCSKVN"

368 c 330 g 237 t

Query Match Best Local

582;

Similarity 62. 92; Conservative

0

Score 341.8; DB 8; Length 1220; Pred. No. 4.8e-40; O; Mismatches 337; Indels 18;

Gaps

2

25.2%;

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REFERENCE
AUTHORS
TITLE
                                                                   SOURCE
ORGANISM
                                                                                                                DEFINITION ACCESSION
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Zea mays
Embryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Andropogoneae; Zea.
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Zea mays putative peroxidase
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On Jul 25, 2001 this sequence version replaced
Location/Qualifiers
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Padegimas, L.S. and R
Direct Submission
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Padegimas, L.S. and Reichert, N.A.
Direct Submission
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Submitted (06-DEC-1997) Department of Plant and Soil Sciences, Mississippi State University, Box 9555, Mississippi State, MS 39762, USA

/translation="MAASVSASCLISLSSLAVVLVALASAASAQLSSTFYDRSCPNAL STIRSGVNSAVRQEPRVGASLLKLHFHDCFVRCDASLLLKDTSGSGOGDHLTLNPR GFVVVNSIKAQVESVCFUSCALKLHFHDCFVRCDASLLLKDTSGSGOGDHLTNASFPGQ TSDPPPTSSLAVAKYNKKNLAPTDMVALSGAHTIGQAQCESFNDHIYNDSTANSAFDASLRANCPRAGSTALAPLDTTTPNAFDNAYYTNLLSQKGLLHSDQELFNNGSTDST PRASLRANCPRAGSTALAPLDTTTPNAFDNAYYTNLLSQKGLLHSDQELFNNGSTDST PRSFASQHVGLQQRLRHGHGQDGQPQPPDRNPGADQAQLLEGQLVNY" P7X"

gi·3925232

Length 1360;

112 CTCTCCTGTGTCGCCCACGCACACGTTCTGCCCCACGTTCTATGCGTCCTCCTGCCCCAAC Score 334.6; DB 8; Pred. No. 5.2e-39; 0; Mismatches 309; 13; Gaps 197 171 Ģ

CTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGC GCGCTGTCCACCATCAGGAGCGGCGTGAACTCCGCGGTGAGGCAGGAGCCTCGCGTGGGG 231 291 257

CTTCT---CGACGCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGC---GC GCGTCGCTGCTCAGGCTCCATTTCCACGACTGCTTTGTCCGGGGCTGCGACGCGTCCCTT

317

GGCTTCGTTGTCGTGAACAGCATCAAGGCGCAGGTGGAGTCCGTGTGCCCGGGGGATCGTC 465 437

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Arabidopsis thalia		21	1186	12.5	169.2	Ü
Arabidopsis thalia	AAC46	21	1073	12.7		4.
Arabidopsis thalia	AAC42	21	1014		٠.	٠ تـ
		21	1247	12.7	172.6	Ñ
Barley BP 1 peroxi	AAZ52	21	938		17	Ξ
Ľ.	AAC47	21	1244		.4	0
۵	AAA68	21	646		.51	9
sativa r	AAH44	22	1204			8
radiata r	AAA68	21	586		.~	37
Lolium perenne Lap	ABN87	24	792		.4	8
perenne		24	787		.4	5
=	ABN87206	24	790		184.6	4
		22	1433		186.4	ũ
sativa		22	1445		190.2	ະ
sativa		22	1370		190.2	ï
santhes		18	1144		210.2	ŏ
		22	1306		210.6	29
sativa		22	1256		213.4	8
ıva		22	1317		216.8	27
sativa per		22	1325		220	8
5 1		20	1355	•	226.6	25
sativa		22	1137	•	231.4	24
sativa r		22	1348	•	233.6	3
۵	AAA68185	21	916	17.3	234	22
sativa		22	1218	•	236.2	21
sativ		22	1233	•	238.8	20
leaf		14	1348	•	240	19
-	AAC3662	21	1220	18.0	243.4	18
va pero	AAH4407	22	1444		244.6	17
-4-	AAC4969	21	1218	•	245	16
unthetic	AAF62	22	975	•	245	15
PTIC NI	AAF6277	22	975		254.4	14
Victor	AAA6817	21	1391	•	258.6	3
radiata r	AAA6819	21	801	•	268.6	12
sativa r	AAH440	22	1250		273	11
Pinus radiata pero	AAA68187	21	1224		274.4	10

ALIGNMENTS

RESULT 1 AAH44077 (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES 08-DEC-2000; 2000WO-JP08728 WO200142475-A1 CDS Oryza sativa Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grises; ss. Oryza sativa AAH44077 standard; cDNA; 1156 BP 10-DEC-1999; 14-JUN-2001. 12-SEP-2001 AAH44077; peroxidase s4235 encoding cDNA SEQ ID NO:13. (first entry) 99JP-0352472. Location/Qualifiers 75..1058 /*tag= a /*tag= a /product= "peroxidase s4235"

Ohashi Y, Hiraga S;

Mitsuhara I,

Sasaki T,

Nagamura Y,

Ito Ħ

Iwai T;

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Best Local Sim
Matches 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA, to a peroxidase set by isolating RNA from the plant, binding the RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New set of rice peroxidase genes for analysis of peroxidase exin rice under varying conditions and production of rice plants desired characteristics \,
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DB; AAB99738.
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                                                                              CGCTCATCTCCCTGTTCGGCAGGCAGGGCCTGTCGCCGCCGGCGACATGACGGCGCTGTCGG
                                                                                                                          GCACGACGAGCCAGAGCGCGAACACCAACCTGCCGCCGCCCGGCGCGAGCCTCGCGT
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                GCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCGGCCGCATCTACGGCGACA 679
                                                            CGCTCCTGTCGATGTTCAGCGCCAAGGGCCTCGACGCGCGGACCTCACCGCGCTGTCGG
Similarity
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Pred. No. 1.7e-70;
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Hiraga S;
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                                           New set of rice peroxidase genes in rice under varying conditions desired characteristics -
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                                                                                P-PSDB;
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DB; AAB99743.
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53..1033
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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and

Claim 1;

Page 183-186; 258pp; Japanese.

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Best Local Similarity 67.2%;
Matches 604; Conservative
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GCACTCCGACCAGGAGCTGTTCAACAACGGGCCGGTGGACTCGGTGGTGCAGCTGTACAG
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Pred. No. 5.9e-68;
0; Mismatches 280; Indels 15
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Query Match Best Local S Matches 592

Similarity

26.6%; 63.1%;

Score 360.8; DB ; Pred. No. 3.1e-60; 0; Mismatches 33;

DB 22; T; 0 other;

Length 1310

Gaps

2;

Conservative

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RESULT 3
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                                                    The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AnH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a cCC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene capression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and conditication of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
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                                 New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics - \footnote{`}
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Claim 1; Page 189-192; 258pp; Japanese.
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The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC presents, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using the CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene component tissues and under different environmental conditions, their component tissues and under different environmental conditions, candidification of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the CC plants such as response to bacterial infection by Magnaporthe grisea.

Sequence 1223 BP; 234 A; 397 C; 338 G; 254 T; 0 other;

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                                                          TTCCGGGGGGAGCAGGGTGCGTTCCCTAATGTCAACTCGCTGAGGGGATTCGAGGTCATC
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Pred. No. 2.6e-59;
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                                                                                  Lolium perenne; perennial ryegrass; plant; cell wall; lignification; cellulase; enzyme; lignin biosynthesis; cellulose degradation; CCOAMT; caffeoyl-CoA 3-O-methyltransferase; cinnamyl alcohol dehydrogenase; CAD; caffeic acid O-methyltransferase; OMT; cinnamate-4-hydroxylase; CCH; cinnamoyl-CoA reductase; CCR; peroxidase; PER; ferulate-5-hydroxylase; P5H; CELL; phenylalanine ammonia lyase; PAL; 4-coumarate:CoA ligase; 4CL; ryegrass; fescue species; molecular genetic marker; gene; ss.
                                                                                                                                                                                                                                                                                                   ABN87249
                              WO200226994-A1
                                                                                                                                                                                                         Lolium perenne peroxidase 1 cDNA sequence SEQ ID NO:176
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CC encoding caffecyl-CoA 3-O-methyltransferase (CCOAMT), cinnamyl alcohol
CC dehydrogenase (CAD), caffeic acid O-methyltransferase (CCOAMT), cinnamyl alcohol
CC cinnamate-4-hydroxylase (CAH), cinnamyl-CoA reductase (CCR), peroxidase
CC cinnamate-4-hydroxylase (FAH), cinnamyl-CoA reductase (CCR), peroxidase
CC cinnamate-4-hydroxylase (FAH), peroxidase
CC cinnamonia lyase (PAL) or 4-coumarate:COA ligase (4CL) from perennial
CC ryegrass (Lollum perenne) or fescue species. (1), its nucleotide
CC sequence information and/or single nucleotide polymorphisms is useful as
CC sequence information and/or single nucleotide polymorphisms is useful as
CC blosynthesis and/or cellulose degradation in a plant to manipulate cell
CC blosynthesis and/or cellulose degradation in a plant to manipulate cell
CC walls. (1) or its fragments are useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, as
CC walls. (1) or its fragment are useful in amplification protocols
CC to amplify longer nucleic acids or its fragments encoding homologous
CC genes from DNA or RNA. (1) or its fragments are useful as molecular
CC genetic markers for quantitative trait loci (QTL) tagging, QTL mapping,
CC tagging QTLs for herbage quality traits, dry matter digestibility,
CC trepital stature, leaf and stem colour. The present sequence represents a
CC Lollum perenne (perennial ryegrass) nucleotide sequence from the present
CC invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding lignification and cellulase enzymes their related enzymes useful for modifying lignin biosynthesis cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 105; 436pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention
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Sequence 1295 BP; 295 A; 420 C; 337 G; 241 T; 2 other;

Query Match Local Similarity Conservative 25.5%; 0; Score 345.6; Pred. No. 2.6e-57;); Mismatches 339; Indels · 12; 1295; Gaps Ψ

QΥ 망 Qy В Qy 밁 Qy Вb QV Вb Ωy Best Loca Matches 364 184 145 304 265 244 205 124 322 85 64 GCCCACGCACACGTTCTATGCGTCCTCCTGCCCAACCTGCAGAGCATC GCCATGGCATCTGCCTCTTGCATTTCTTTGGTGTTGCTGGTGGCCCTGGCAGCCACGGCG 144 GCCATGGCGTCTCCCACCTTGATGCAATGCCTGGTCGCCGTTTCCCTCCTCTCTGTGTC 123 ACCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTGTGCGCCGACATCCTC GGCAACGAGCAGAACGCGCCTGCGAACGCCGGTTCGCTGTTTGGCTTCGGCGTCATCGAC GGAGGGGAGAAGACCGGCCGGGCCGAACCTGAACTCGGTGCGCCGGCTTTGAGGTCATCGAC AGGCTGCACTTCCACGACTGCTTTGTTAATGGCTGTGACG---CGTCCGTTCTGCTGTCG ATCAAGAGCGGCGTGGCAGCCGCGTGAGTAGCAACCCCCGCATGGGCGCGTCGCTGCTC GTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTC GCGTCGGCGCAGCTGTCGACGTTCTACGACACGTCGTGCCCCAGGGCCCTGGCCACC 423 363 321 303 264 243 204 183 381

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GCGCTTGCCGCGCGACGGAACCAACCTTCTCGGCGGGCCGACCTGGAGCGTGCCGCTC

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                                                                                                                                                                                    Oryza sativa
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                                                                                                                                                                                                                                          Oryza sativa peroxidase r3025 encoding cDNA SEQ ID NO:19.
                                                                                                                                                                                                                                                                 12-SEP-2001
                                                                                                                                                                                                                                                                                       AAH44080;
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 Ohashi Y,
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                     (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                            10-DEC-1999;
                                                                 08-DEC-2000;
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 Mitsuhara
                                                                  2000WO-JP08728
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                                                                                                                                                                                                          rice; plant;
                                           99JP-0352472
                                                                                                                                 /*tag= a
/product=
                                                                                                                                                       Location/Qualifiers 14..997
                                                                                                                                           /*tag=
                                                                                                                                                                                                            peroxidase; POX; characteristic; gene expression;
bacterial infection; Magnaporthe grisea; ss.
                                                                                                                                                                                                                                                                                                           1158
  Sasaki T,
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Query Match Best Local Sim Matches 580;

Local Similarity

25.0%;

Score 338.6; Pred. No. 5.6

DB 22; Length 1158;

pred. No. 5.6e-56;
0; Mismatches 339; Indels

18;

Gaps

2

Conservative

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fragments, where the sequences of the peroxidase genes in the set are control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene capters of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specification of rice plants to provide desired specifications of the peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 171-174; 258pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New set of rice peroxidase genes in rice under varying conditions desired characteristics -
Sequence 1158 BP; 255 A; 322 C; 327 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                         The present invention describes a set of peroxidase genes four plants, especially rice, and their homologues, modified forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for analysis of peroxidase expression and production of rice plants with
                                                                                                                                                                                                                                                                                                                                                                                            found
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В δÃ δÃ 밁 οy 밁 Q 밁 ρy 밁 Qy 밁 δÃ В QΥ Qy В δÃ В 믕 108 588 468 482 408 422 348 362 288 302 228 254 168 194 134 542 48 74 CTCCCACCTTGATGCAATGCCTGGTCGCCGTTTCCCTCCTCTCTGTGTCGCCCACGCAC 133 crecceccreercereareereereereerecreeceereeceeceereereere TTGGTCGGAGACTCGCGCACGGCGAGCCTCAGCGGCGCAAACAACAACATCCCGCCGC TCGGGCGGGGACTCGACGACGGCCAGCGCCTCGCTGGCCAACAGCAACCCCCCCGCCCC TCGCGCTTGCCGCGCGCGACCGAACCTTCTCGGCGGCCGACCTGGAGCGTGCCGC ACACCATCAAGCGGAACGTCGAGGCCGCGTGCCCGGCGTGTCGTGCGCCGACATCC TCCACGACTGCTTCGTCCAAGGTTGCGACGCATCGCTGCTGCTGGACGACACGGCGAGCT TCCACGACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACG-----GGATGCAGTCGGCCATCGCCAGGGAGAAGCGCCATCGGCGCCTCCATCGTCCGCCTCTTCT AGCTGTCGCCGAGCTTCTACTCGTACTCGTGCCCGGGAGTGTTCAACGCGGTGAAGCGGG 167 AGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGG 193 ACATGGTCGCCCTCTCCGGATCTCACACCATTGGGCAAGCACGATGCACAAACTTCAGAG ACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCTTCCGCG 287 481 407 421 347 361 301 647 661 601 541 467 587 527

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                                                                       The present sequence represents the cDNA sequence of a peroxidase P7X gene. The P7X gene is isolated from maize inbred line Mp307. Peroxidases reduce hydrogen peroxide or molecular oxygen in the presence of an electron donor. Plant peroxidases are involved in pathogen defence responses. DNA constructs or transcription cassettes comprising peroxidase P7X gene and its promoter are useful for providing nematode resistance in plants.
                                                                                                                                                                              Claim 1; Fig 3; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF90234 standard;
                                                  Sequence 1379
                                                                                                                                                                                                                Novel gene encoding peroxidase P7X protein, and its promoter, useful for producing transgenic plants that are resistant against nematode
                                                                                                                                                                                                                                                          WPI; 2001-355920/37
                                                                                                                                                                                                                                                                                 Padegimas LS,
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Hiraga S;
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P-PSDB; AAB99742.
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; bacterial infection; Magnaporthe gris
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                                                                                                                                                                                                                                                Score 314.4; DB Pred. No. 2.5e-50; Mismatches 2
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                                                  GATGGCCAGCCTGAGCCCGCTCGTCGGGAGCCAAGGCGAGGTCCGCGTCAACTGCAGGAA 1074
                                                                            GATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGATCAGGCGCAACTGCCGGGT
                                                                                                     CAGGTTCTACGCCGCCAACCCGGACGCGGTTCCGGCGAGACTTCGCCGAGTCCATGGTGAG
                                                                                                                                                           CCTGCACTCGGACCAGCAGCTGTTCGCCGGCGGCGGCCTCGGCGCCCACCGACGGGCTCGT
                                                                                                                                                                                                                                                                   CGGGGGGACCTGCCCGCGTACCGCCGGCGCGCGACGACAACCTCGCGCCGCTCGAC--
                                                                                                                                                                                                                                                                                                                      CTTCCGCGACCGCCTCTACAACGAGACGGCCACGCTCGACGCCTCGCCTCGCCGTCGCT
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RESULT 9
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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lignin biosynthetic pathway; Eucalyptus grandis; Monterey pine; ds.
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99US-0143811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polynucleotides and proteins cencoding and representing the enzymes cinnamate 4-hydroxylase (C4H).-CC commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (C4T), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-coA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase (4CL), CC coniferol glucosyl transferase, caffecyl co. coniferin beta-glucosidase (CBC), coniferin beta-glucosidase (CBC), CC cafeic acid methyl transferase, caffecyl COA methyl transferase, caffecyl COA methyl transferase, close, commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol commostition and the structure of a plant, especially eucalyptus and pine composition and the structure of a plant, especially eucalyptus and pine content, composition and structure of a plant, especially eucalyptus and content, composition and structure. They can be used for designing probes can be useful for detecting similar DNA and RNA sequences in any cransism and for PCR amplification. The lignin content can be efficiently composition and the polynucleotides. AAA67908 to AAA68201 and AAB16341 to CC exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
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                                                                                                                       ACATTCTCGCCATTGCTGCTCGTGATTCTGTTGAACTGGGCGGTCCTTCATGGACAG
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                                                      TAATGTTGGGAAGGCGAGACTCGACAACAGCTAGCAAAAGCGGTGCAAACAGTAATATTC
                                                                                       TGCCGCTCGGGCGGCGGGACTCGACGACGGCCAGCGCCTCGCCCAACACAGCAACCCCC
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59.7%;
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14-JUL-1999;
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                                                                                                                                    WPI; 2000-317962/27
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                                                                                                                                                          LN,
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                                                                                                                                                                                                                                                                                                                                          lignin biosynthetic pathway; Eucalyptus grandis; Monterey pine; ds.
                                                                                                                                                          Havukkala
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99US-0143811.
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The present invention describes isolated polynucleotides and protein encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), C-methyl transferse (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase

s and proteins (ylase (C4H), transferase

Claim 1; Page 187-188;

213pp; English.

Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and

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laccase, peroxidase, ferulate-5-hydroxylase (FH), alpha-amylase, caffelc acid methyl transferase, caffeoly coa methyl transferase, counterate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase, which are involved in the lighth biosynthetic pathway. The polynucleotides can be used for modulating lighth content, lighth composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighth biosynthetic pathway, and for producing a plant having altered lighth content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any crganism and for PCR amplification. The lighth content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB.6341 to AAB16449 represent polynucleotides. AAA67908 to AAA68201 and AAB.6341 to Cambification of the present invention.
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ACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTGAGGCAGTACAGCGCCAGCG 895
                                                   TCACATTTGACAACAAGTATTACTCTAATCTTAAAATACAGAAAGGACTTCTCCACTCCG
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                                                                                                         TGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGCGGGCCGGTTTCCACTCGG
                                                                                                                                                                                                                                                                               TCAGAACTCGGATCTACAACGAAACGAACATTAACGCTGCTTTCGCTACATCTGTAAAGG
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Pred. No. 1.2e
0; Mismatches
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les 356; Indels
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                                                 The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC expression analysis. The set of genes are used for the analysis of the CC expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grisca; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 220-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics - ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000; 2000WO-JP08728
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Query Match
Best Local Similarity

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GGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGATCAGGCGCAACTGCCGGGTCGT 998
                                                                                                                                                                                                GCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGACTTCGTGGCAGCCATGATTAGGAT 938
                                                                                                                                                                                                                                                                             GGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTGAG
                                                                                                                                                                                                                                                                                                                                                            CCCTCCGGCCGCCGACGGCAACGTCTCCGTCGCCCAGGACGCCATCGACAACCTCCC
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                                                                                                                      GGGGAGCATCGAGGTGCTCACCGGCAGGCCAGGGCGAGGTCAGGCTCAACTGCAGCGTCGT
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ilarity 58.4%;
Conservative
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Pred. No. 2.2e-43;
0; Mismatches 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1250;
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                                                                                                                                                                                                                                                                    The present invention describes isolated polynucleotides and proteins comparate 3-hydroxylase (C4H), Commarate 3-hydroxylase (C5H), phenolase (PNL), O-methyl transferase (C6MT), cinnamyl alcohol dehydrogenase (PNL), Commarate: C6A reductase (C6R), phenylalanine ammonia-lyase (PAL), 4-commarate: C6A reductase (C6R), phenylalanine ammonia-lyase (PAL), 4-commarate: C6A reductase (C6R), phenylalanine ammonia-lyase (PAL), 4-commarate: C6A reductase (C6C), C6C coniferol glucosyl transferase, C7, coniferin beta-glucosidase (C6G), C7, coniferin beta-glucosidase (C6G), C7, conferin beta-glucosidase (C6G), C7, coniferin coniferin beta-glucosidase (C6G), C7, coniferin beta-glucosidase (C6G), C7, coniferin coniferin beta-glucosidase (C7, coniferin coniferin beta-glucosidase (C7, 
                                                                                                                                                         Query Match
Best Local Similarity
Matches 464; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis; Pinus radiata; Monterey pine; ds.
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                                                                                                                                                                                                                                        Sequence 801 BP; 195 A; 217 C; 195 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 189; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloksberg LN, Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                  CCTGGTCGCCGTTTCCCTCCTCTGTGTCGCCCACGCACAGCTCTCGCCCACGGTTCTA 152
                                                                            Conservative ·
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99US-0143811.
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                                                                                                                                                         19.8%; Score 268.6; DB 21; Length 60.7%; Pred. No. 1.5e-42; tive 0; Mismatches 289; Indels
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RESULT 12 AAA68192 ID AAA68 XX

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                                                                                       09-OCT-1998;
14-JUL-1999;
                               Bloksberg LN, Havukkala
                                                                                                                       06-OCT-1999;
                                                                                                                                                                                     Eucalyptus grandis
                                                                                                                                                                                                           Pinus radiata;
                                                                                                                                                                                                                                            Eucalyptus grandis peroxidase nucleotide sequence SEQ ID NO: 352.
                                                                                                                                                                                                                                                                                                             AAA68176 standard;
                                                      (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                            20-APR-2000.
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                                                                                                                                                                                                            Monterey
                                                                                                                                                                                                                      lignin biosynthetic pathway;
                                                                                      98US-0169789.
99US-0143811.
                                                                                                                       99WO-NZ00168
                                                                                                                                                                                                                                                                                                             1391
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Novel polynucleotide encoding enzymes involved in lighth-biosynthetic pathway useful for producing transgenic plants especially encalyptus and pine species having altered lighin content, composition and structure

Claim 1; Page 184; 213pp; English.

CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (CMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-coA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CAD), coniferin beta-glucosidase (C8G), CC caffeic acid methyl transferase, caffeoyl cOA methyl transferase, CC coumerate COA ligase, cytochrome p450 LXXIA, diphenol oxidase, flavanol qlucosyl transferase, flavanol hydroxylase, and isoflavone reductase, CC which are involved in the lighin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC polynucleotides can be used for modulating lighin content, lighin CC composition and the structure of a plant, especially eucalyptus and pine CC polynucleotides, and for modifying the activity of an enzyme involved in lighin CC content, composition and structure of a plant, especially eucalyptus and pine CC polynucleotides, and for producting a plant having altered lighin CC content, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DNA and RNA sequences in any cc modified using the polynucleotides. AhA67908 to AhA68201 and AhAB16341 to AhAB16445 represent polynucleotides and protein sequences used in the cCC exemplification of the present invention.

Sequence 1391 BP; 399 A; 321 C; 307 G; 364 T; 0 other;

Length 1391;

В QΥ 뫄 QY밁 γQ 망 QY B Qy 멍 QΥ В Qy 망 Ş DЬ Query Match Best Local S Matches 505 652 472 600 412 540 352 480 300 420 360 184 300 124 GCCCACGCACAGCTTCCCACGTTCCTATGCGTCCTGCCCCAACCTGCAGAGCATC 720 244 Match 19.1%; Local Similarity 56.7%; GTTCGGGCGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTC ACCITCCGCGGCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCCGCGGCGCTGCGG GAAGTGATCGACCGCATCAAGGCTAGTCTGGAGAAGGAGTGCCCTGGAGTGGTTICCTGT GAGGTCATCGACACCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGC CGGCTGCACTTCCATGACTGCTTCGTCAATGGGTGCGATGCGTCGATATTGTTGGATGAC GCCCGTTGTAAGCTCTCACCGAGTCATTATCAATCAACATGTCCGAAAGCATTGTCGATT TCGCCGCGCGACATGACGGCGCTGTCGGGCGCGCCACCATCGGGCAGGCCCGGTGCACC ATACCTCCACCTACTTCTAATCTCAGTGCTCTCATAACCAGCTTCGCTGCTCAGGGTCTT ACCGTAAGCTTAGGGAGAAAGGATTCCATTACTGCTAGCAGGAGCCTTGCTAAÇACCTCC GCAGATATCGTTGCCCTGGCTGCTCGCGACTCAGTCGTTCATTTGGGAGGTCCTTCATGG 505; Conservative Pred. No. 1.3e-40;
0; Mismatches 374; Score 258.6; DB 21; Pred. No. 1.3e-40; Indels 12; Gaps 359 651 591 719 471 599 411 351 479 419 243 183 711 659 299 ۲,

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The present sequence is a synthetic Nicotlana sylvestris peroxidase gene which is optimised for expression in plants. The sequence may be introduced into plants to produce insect-resistant plants, preferably maize. It is useful for controlling insects such as ostrinia nubilalis, Heliothis zea and Spodoptera frugiperda. The transgenic seeds and plants can be used for the breeding of improved plant lines which, for example, increase the effectiveness of conventional methods such as harbicide or pesticide treatment or allow the conventional methods to be dispensed with. The peroxidase enzymes can be used in multiple insect control strategies, resulting in maximal efficiency with minimal impact on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
Heliothis
                                                                                                                                                                                                                                                Novel anionic peroxidase genes isolated from Nicotiana tomentisiformis and anionic peroxidase protein encoded by the genes, useful for producing plants resistant to insects -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco; Nicotiana sylvestris; peroxidase; insecticide; transgenic plant; insect-resistant plant; Ostrinia nubilalis;
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                                                                                                                                                                                                                Claim 19; Page 54; 58pp; English.
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16-NOV-1999;
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Pred. No. 8.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco; Nicotiana tomentisiformis; peroxidase; insecticide;
transgenic plant; insect-resistant plant; Ostrinia nubilalis;
Heliothis zea; Spodoptera frugiperda; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel anionic peroxidase genes isolated from Nicotiana tomentisiformis and anionic peroxidase protein encoded by the genes, useful for producing plants resistant to insects \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic Nicotiana tomentisiformis peroxidase gene.
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16-NOV-1999;
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pred. No. 5.1e-38;
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CGAGATCCGCACCGACTGCAAGCGCGTGAAC
              ACAGATCAGGCGCAACTGCCGGGTCGTCAAC 1002
                                                                                                   CGGCAGCGCCACCATCGCCATCGTGAACCGCTACGCCGGCAGCCCAGACCCAGTTCTTCGA
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Result
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SOFTWARE: Fast
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                                      Query Match
Best Local Similarity 58.1
Matches 510; Conservative
                                                                                                          TYPE: DNA
ORGANISM: Pinus
-09-615-192A-363
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APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Modification of Plant Lignin
TITLE OF INVENTION: Modification of Plant Lignin
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR EILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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CURRENT APPLICATION NUMBER: US/09/615,192A
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                                                                                                                                          Sequence 368, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION:
    TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant FILE REFERENCE: 11000.1003c4U CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21
                                                                                                               APPLICANT: Bloksberg, APPLICANT: Havukkala,
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PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 368
LENGTH: 801
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-368
RESULT 4
US-09-615-192A-352
; Sequence 352, Application US/09615192A
; Patent No. 6410718
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Matches 464; Conservative
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                                                                                CAACCTGCTGTCGCGGGCGGGGCCTGTTCCACTCGGACCAGGAGCT 845
                                                                                                               CGACATCAACGCCTCCTTCGCGGGGGCGGCGGCGGCAGACGTGCCCGCGGGGGCGACGAA
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Pred. No. 1.6e-47;
0; Mismatches 289; Indels 12;
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003-04U
CURRENT APPLICATION NUMBER: US/09/615.192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1391
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CCGACCTTCTTTGACAACCTTTACTACCACAATTTACTGCAGAAGAAGGGCCTTCTTCAC
                                        CCGGTGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGGCCTGTTCCAC
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APPLICANT: Lagrimin1, Mark

APPLICANT: Desa1, Nalin1

FILE OF INVENTION: No. 6278041el Peroxidase Gene Sequences

FILE REFERENCE: S-31081p1

CURRENT APPLICATION NUMBER: US/09/365,150

CURRENT FILING DATE: 1999-07-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 975

TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 58.3
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                                                                                                                   CCTTCTCGACGCCGGAGGGGAGAAGACC-----GCCGGGCCGAACCTGAACTCGGTGCG 344
                                                                                                                                                                                                                                                                                                                                     CGCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAACGGCTGCGACGGCAGCAT
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                                                                                                                                                   GAGCTGCGCCGACATCCTGGCCCTCGCGAGCGAGATCGGCGTGCTGGCCAAGGGCCC
                                                                                                                                                                                                              CGGCTTCGACATCGTGGACGACATCAAGACCGCCCTCGAGAACGTGTGCCCCCGGAGTGGT
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Pred. No. 1.6e-44;
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: tomentisiformis peroxidase gene
US-09-365-150-4
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US-09-365-150-4
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CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 975
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09365150
Patent No. 6278041
GENERAL INFORMATION:
APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6278041el Peroxidase
FILE REFERENCE: S-31081P1
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                         111 CCTCTCCTGTGTCGCCCACGCACAGCTTCTCGCCCACGTTCTATGCGTCCTGCCCCCAA 170
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                                                                           CGCCTCTCTGCTCAGGCTCTTCCTTCCACGACTGCTTCCAAGGCTGCGACGGATCGAT
                                                                                                                           CATCTTCGCCGCCAGCAACGCCCAGCTGAGCGCCACCTTCTACGACAGCACCTGCCCCAA 104
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CCTGCTGGACACCGACGCACCCAGACCGAGAAGGACGCTGCTCCCAACGTGGGCGCCG-
                                                            CGCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAACGGCTGCGACGGCAGCAT
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                  18.1%; Score 245; DB 4; 58.4%; Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                    Mismatches 345;
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RESULT 7
US-09-615-192A-361
                                                                        CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
              SOFTWARE: Fa
SEQ ID NO 361
LENGTH: 916
                                                                                                                                                                                                      Sequence 361, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, IIkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000.1003c4U
                                                           NUMBER OF SEQ ID NOS:
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                                             FastSEQ for Windows Version
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                                                                                                                                          Sequence 5,
Patent No. (
                                                                                         APPLICANT: Ainley
APPLICANT: Armstr
            APPLICANT:
APPLICANT:
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APPLICANT:
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, Application US/09097319A 6384207

Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.

Armstrong, Ka Belmar, Scott Ainley, Michael

Katherine

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; ORGANISM: Pinus radiata US-09-615-192A-361
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Best Local Similarity 58.7%;
Matches 452; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 CCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGGCGATGACCC
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TCTTCAACGGAGGCTCCACTGATTCGCATGTGACTAAGTACGCCTCCAAC
                                                                                                                                          CACAGGCTCCGGAGACAGCAACCTGTCGCCACTGGATTATACGACTCCCACTGTGTTTG
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                                                                                               ACACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGC
                                                                                                                                                                                  C-----CGGCGGCGACGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCG
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Pred. No. 2.7e-40;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
HOLECULE TYPE: DNA
US-09-097-319A-5
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Best Local :
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NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ. ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
621
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CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                TGACGGCGCTGTCGGGCGCGCACCACCATCGGGCAGGCCCGGTGCCACCACCTTCCGGGCCC
                                                                             GGGGGGGGACTCGACGACGGCCAGCGCCTCGCCAACAGCAACCCCCCGCCCCGA 544
                                                                                                                                                                                                               CGCTTGCCGCGCGCGACGGAACCAACCTTCTCGGCGGGCCGACCTGGAGCGTGCCGCTCG 484
                                                                                                                                                                                                                                                AGATTAAGGCTGCTCTTGAGGCTGCCCTGCCCAGGCACAGTCTCCTGTGCCGACATTGTTG
                                                                                                                                                                                                                                                                  CCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCCGACATCCTCG
                                                                                                                                                                                                                                                                                                                           GAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACA 364
                                                                                                                                                                                                                                                                                                                                                                                      ACGACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACGCC------G 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTCGCCCTCTCAGGTGGTCACACCATTGGTATGTCTCGGTGCACTAGTTTCCGGCAGA 680
                                                           ACAACACTCCCCACTATCATCACCAAGTTCAAGCGCCCAGGGCCTCAATGTTGTTGATG
                                                                                                                      GCCGGAGAGACTCGCTCGGTGCAAGCATCCAGGGCTCCAACAATGACATCCCAGCCCCCA
                                                                                                                                                                                   CCCTTGCGGCTCGTGATTCCACCGCCCTGGTTGGTGGACCATACTGGGACGTGCCACTTG
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Pred. No. 1.1e-38;
0; Mismatches 359;
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APPLICANT: BLOKSberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Cont
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 586
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Query Match 13.5%; Score 182.8; DB 4; Best Local Similarity 61.2%; Pred. No. 1.2e-29; Matches 295; Conservative 0; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                        GCCCGGTGCACCACCTTCCGCGGCCGCATCTACGGCGACACCGACATCAA:GCCTCCTTC 699
                                                                                                                                                  AGGCAGGGCCTGTCGCCGCGCGACATGACGGCGCGCTGTCGGGCGCGCACACCATCGGGCAG 639
  GCGGCGCTGCGGCAGCAGACGTGCCCGCGGCGGTCCGGCGGCGACGGCAACCTGGCGCCCCATC 759
                                        GCACGGTGCACCACATTCAGAACTCGCATCTACAACGATACCAACATTAACGCTGCCTTC 180
                                                                                                              AAACAGGGTCTCTCTACCAAGGACCTCGTCGCACTCTCAGGTGCTCATACAATTGGTCAA 120
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-365
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION UNMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR TILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILIN
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Best Local Similarity 58.0
Matches 331; Conservative
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APPLICANT: Bloksbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 365, Application US/09615192A Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin (FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000 AA 1001
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CCAACAACAATTCGTTGAGGGGTTTCGACGTCATAGACACCATCAAATCACAAGTGGAAG
                                       CGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGG 385
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58.6%;
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Pred. No. 3.4e-28;
0; Mismatches 222;
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US-09-615-192A-359
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SEQ ID NO 359
LENGTH: 659
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Best Local Similarity 54.6
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR ETLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR ETLING DATE: 1996-09-11
PRIOR PPLICATION NUMBER: US 09/169,789
PRIOR ETLING DATE: 1998-10-09
PRIOR ETLING DATE: 1998-10-09
PRIOR ETLING DATE: 1998-10-09
PRIOR ETLING DATE: 1998-10-09
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APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
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  GACGGAACCAACCTTCTCGGCGGGCCGACCTTGGAGCGTGCCGCTCGGGCCGGGCCGGGACTCG
                                      TTGGAGGAAGCATGTCCTGGAGTGGTCTCATGTGCTGACATTCTTGCTGGCAGCCCGT
                                                               GTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCGACATCCTCGCGCTTGCCCGCGCG 438
                                                                                                              GCATTACCTAACAGAATTCTGTAAGAGGCTTTGAGGTAGTGGATAAGATCAAAAGCAAA 395
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GENERAL INFORMATION:

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TITLE OF INVENTION: IC NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:

STREET: 10 S. CITY: CHICAGO

ADDRESSEE

COUNTRY: U.S.A.

60606 ILLINOIS

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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quence 9, Application US/08190029A
tent No. 5736363
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APPLICATION NUMBER: GB 9116325.3
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10 S. WACKER DRIVE, SUITE 3000
                                                                                                                                                                                   linear
E: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richard Mark
                      /codon_start= 11
/function= "Gene for IGF-II/HRP fusion protein"
/product= "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB 9202401.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT/GB92/01389
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; LOCATION: 857..1057
; OTHER INFORMATION: /fur
US-08-190-029A-9
                                                                                                  Sequence 9, Applicati
Patent No. 5854025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 304
APPLICANT: EDWARDS, Richard Mark
APPLICANT: BANDEN, Lindsey
TITLE OF INVENTION: IGF-II ANALOGUES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TTCCGCACTGAAAAGGATGCATTCGGGAACGCTAACAGCGCCAGGGGGCT"TCCAGTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Sin
hes 304;
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 1..6
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                                                                                                                                                                                                                                                                                               CGCGGCCGCATCTACGGCGACACCGACA 685
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                                                                                                                                                                                                                                                                                                                                           AGTGACCTTGTGGCTCTGTCCGGAGGACACACATTTGGAAAGAACCAGTGTAGGTTCATC
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                                                                                                                                                   Application US/08462695
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(fragment)"
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Pred. No. 2e-16;
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TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs

FILING DATE: 29-JUL-1991 ATTORNEY/AGENT INFORMATION:

NAME: JOHN J. MCDONNELL REGISTRATION NUMBER: 26

REFERENCE/DOCKET NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/ FILING DATE: 27-JUL-1992

APPLICATION NUMBER: GB 9 FILING DATE: 05-FEB-1992

PRIOR APPLICATION DATA:

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 28-FE

28-FEB-1994

CURRENT APPLICATION DATA:

MOLECULE TYPE: ORIGINAL SOURCE:

ORGANISM:

Homo sapiens

STRANDEDNESS:

double

nucleic acid

ropology:

OTHER INFORMATION: OTHER INFORMATION:

INFORMATION:

LOCATION:

11..1057

NAME/KEY: CDS

STREET: LV _
CITY: CHICAGO
CTATE: ILLINOIS
TIS.A.

ADDRESSEE: BANNER & ALLEGRETTI, LTD. STREET: 10 S. WACKER DRIVE, SUITE 3000

COUNTRY: U.S.A. ZIP: 60606

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                                     Query Match
Best Local Similarity
Matches 304; Conserv
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NFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9116325.3 FILING DATE: 29-JUL-1991 ATTORNEY JARSHY INFORMATION: NAME: JOHN J. MCDONNELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9202401.7 FILING DATE: 05-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/190,029
FILING DATE: 28-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               NAME/KEY: misc_feat
LOCATION: 11..856
OTHER INFORMATION:
OTHER INFORMATION:
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133 CAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCG 192
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                         NAME/KEY: misc_feature LOCATION: 857..1057 OTHER INFORMATION: /fu
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /function= "HinDIII cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                   OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                     Conservative
                                                                                                                                                                                                                                                    misc_feature
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1..6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: PCT/GB92/01389
27-JUL-1992
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                                                    53.5%;
                                                                                                                                                                                               /function= "HRP coding sequence
(fragment)"
                                                                                                                                                                                                                                                                                     /function= "EcoRI cleavage site"
                                                                                                                       /function= "IGF-II coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start= 11
/function= "Gene for IGF-II/HRP fusion protein"
/product= "Synthetic DNA"
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                                                    Score 119.6; DB 2; Pred. No. 2e-16;
                                     Mismatches
                                   249;
                                   Indels
                                                                    Length 1072;
                                 15;
                                 Gaps
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                                                                                                                                                                                             SOFTWARE: I
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 371, Application US/09615192A Patent No. 6410718
                                                                  Matches
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2000-0
PRIOR APPLICATION NUMBER: UPPRIOR FILING DATE: 1997-11-
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                        PRIOR EILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Materials and Methods for the
                                                                                                                                            LENGTH: 1522
TYPE: DNA
ORGANISM: Pinus radiata
182 CTTTCTTGGACGTTCTACAGCTCGAGTTGCCCGTCCTTGGAGTCCATAGTGTGGGAGCGC 241
                               136 CTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGGCG 195
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Havukkala, Ilkka
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TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin C FILE REFERENCE: 11000.1003cAU CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000
                                                                                                                                                                      Sequence 370, Application US/09615192A Patent No. 6410718
                                                                                                                          APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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US-09-615-192A-370
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BG841858 MEST27-D0
BG842311 MEST29-D0
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ALIGNMENTS

	COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 AA979912
Schnable laboratory Iowa State University G405 Agronomy, Ames, IA 50011, USA Tel: (515)-294-0975 Fax: (515)-294-2299 Email: schnablediastate.edu PCR PRIMERS FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3') BACKWARD: Ty-YJ (5'-TAATACGACTCACTATAGGGC-3') Plate: MEST3 row: D column: 6 Seq primer: tw1412 (5'-GAAGATACCCCACCAAACC-3').	Contact: Schnable, PS	Unpublished (1997)	Expressed Sequence Tags from B73 Maize Seedlings	Wen, T.J., Ashlock, D.A. and Schnable, P.S.	1 (bases 1 to 848)	clade; Panicoideae; Andropogoneae; Žea.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	Eukarvota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:	Zea mays	Zea mays.		AA979912.1 GI:3157290 :	AA979912	MEST3-D6.TW1412.Seq ISUM2 Zea mays cDNA clone MEST3-D6 5', mRNA	

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BG841858
BG841858.2
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                                                BG841858 446 bp mRNA linear EST 29-MAY-2001 MEST27-D09.T3 ISUM4-TN Zea mays cDNA clone MEST27-D09.3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /notes Organ: green seedlings; Vector: pAD-GAL4; Site_1: fcoRI; Site_2: xhoI; ds cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an xhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAp lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."

62 a 284 c 236 g 147 t 19 others
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/dev_stage="Two-leaf-stage green sec
/lab_host="XL1-MFR Blue"
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/clone_lib="ISUM2"
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/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schnable Laboratory

Iowa State University
G405 Agronomy, Iowa State University, Ames,
Tel: 515-294-0975
Pax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14208180.
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Zea mays
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/clone_lib="ISDM4-TN"
/tissue_type="Seedling and silk"
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/cultivar="B73"
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                           677 ACACCGACATCAACGCCTCCTTCGCGGCGCCTGCGGCAGCAGACGTGCCCGCGGTCCGGCG 736
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291;
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975
Fax: 515-294-2299
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)...
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                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          State University
                                                      Conservative
                                                                                                                 /clone="MEST29-D08"
/clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:14244343
                                                                 17.8%;
99.7%;
                                                   Score 241; DB Pred. No. 0; 0; Mismatches
                                                                              DB 12;
                                                                           Length 538;
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MEST29-D08
                                                     Indels
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08.3', mRNA
                                                     0;
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                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGC 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 230)
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T18410.1 GI:474233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. 26, 1085-1101 (1994)
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                                                                                                                         Seq primer:
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                                                                                                                                                                Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                  Interdisciplinary Center for Biotechnology DNA Sequencing Core University of Florida
                                                                                                                                                                                                                                                                                                                                                                                  Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
                                                                                                                                                E-mail: robferl@nervm.nerdc.ufl.edu
                                                                                                                                                                                                                                    P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                               E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                     Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Plant Sciences, University of Arizona,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing and mapping of clones
/db_xref="taxon:4577"
/clone="6c02d10"
                                       /organism="Zea mays"
/strain="B73"
                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCCCACCTTGATGCAATGCCTGGTCGCCGCTTTCCCTCCTCCTCTGTGTCGCCCACGCA 132
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MEST3-D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags
Unpublished (1997)
Contact: Schnable, PS.
Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                               FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
Plate: MEST3 row: D column: 6
Seq primer: POLYT-N (5'-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT(AGC)-3').
                                                                                                                                                                                                                                                                                                                 PCR PRimers
FORWARD: tw
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                                                                                                                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 850)
                                                                                                                                                                                                                                                                                                                                                                      State University
Agronomy, Ames, IA 50011,
(515)-294-0975
(515)-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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82 c 60 g 48 t 3 others
                                   /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green see
/lab_host="XL1-MFR Blue"
                                                                                                                         /organism="Zea mays",
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST3-D6"
  /note="Organ: green seedlings; Vector: pAD-GAL4;
EcoRI; Site_2: XhoI; ds-cDNA molecules were gener
                                                                                                                                                                                                                           Location/Qualifiers
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/lab_host="DH10B"
                                                                                                   /clone_lib="ISUM2"
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Pred. No.
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GAL4; Site_1:
   generated as
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62
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                              73 TCTCCCACCTTGATGCAATGCCTGG
                                                                             GCTTAAGCAAGTAGCTTCATTCACCGAGCGTGCAGGCACAGGCAGCAGCTTGCCATGGCG
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TCTCCCACCTTGATGCAATGCCTGG
                                                               GCTTAAGCAAGTAGCTTCATTCACCGAGCGTGCAGGCACAGGCAGCAGCTTGCCATGGCG
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BM501068.1
EST.
                                                                                                                                                                                                                                                                                                                                     Trait and Technology Development, Food and F
Pioneer Hi Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston,
Tel: 515 270 5934
Fax: 515 254 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
Zea mays
Zea.

1 (bases 1 to 383)
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PAC0000000000933 Pioneer
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Jung R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunter, B.G., Beatty, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize opaque endosperm mutations create extensive changes
                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                       rudolf.jung@pioneer.com
.Location/Qualifiers
1. .383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an Xhol oligo-dT primer. The selected pNA:RNA hybrid was treated with RNASE H and us as a template for DNA POLI-catalyzed second strand synthesis. After the addition of Econd adaptors, the ds-cDNAs were disested with Xhol and size-selected. The resulting molecules were directionally cloned into the EcoRI and Xhol sites of the HybrizAP lambda vector (Stratagene) and excised as PAD-GAL4 phagemids." a 226 c 210 g 194 t 52 others
                                                                                                                                                                                                       /organism="Zea mays"
/db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"
/clone_"Yector: pSport1; Site_1:
/note="Yector: pSport1; 77 t
                                                                                                                                           6.3%;
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                                                                                                                               Mismatches
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Ys cDNA,
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AUTHORS
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JOURNAL
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     TITLE
                                       AUTHORS
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                                                                                                                                                                                                    BE597204 436 bp r
PI1_69_D10.91_A002 Pathogen induced
mRNA sequence.
BE597204
                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC · clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 436)
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Sorghum bicolor
                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
                                                                                                                         Sorghum bicolor
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                                                                                                                                                                  BE597204.1
EST.
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Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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An EST database from Sorghum: dark-grown seedlings
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 404)
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DG1_86_C05.g1_A002 Dark Grown
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EST database from Sorghum: pathogen-induced plants
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706 583 0210
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a 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
127 c 122 g 68 t
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/db_xref="taxon:4558"
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100.0%;
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Pred. No.
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Pred. No. 0;
Mismatches
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n 1 (DG1) Sorghum bicolor cDNA,
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d 1 (PI1) Sorghum bicolor cDNA,
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Best Local S
Matches 76
                                                              TITLE
                                                                                                   AUTHORS
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Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and I
                                                                                                   Cordonnier-Pratt, M.-M.,
                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 471)
                                                                                                                                                                                                       Sorghum bicolor
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DG1_85_C06.g1_A002 Dark Grown
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Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                           An EST database from Sorghum:
                                                                                                                                                                                                                         sorghum
                                                                                                                                                                                                                                                                      BE362317.1
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/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inculation:
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Collectorichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."

97 a 135 c 127 g 77 t
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/db_xref="taxon:4558"
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                                                                                                   Gingle, A.,
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                                                           dark-grown seedlings
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(DG1) Sorghum bicolor
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                                                                                                      Sudman, M.
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or cDNA, mRNA
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aceae; PACC
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Sequences have been trimmed
below Phred quality 16. The
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                                                                                      High quality sequence start: 4 High quality sequence stop: 443
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Sequences have been trinumed
below Phred quality 16. The
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Fax: 706 583 0210
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 471)
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PI1_69_G08.g1_A002 Pathogen induced 1 (PI1)
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                                                                                                                              primer: PolyTMix
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Lambda Zap; Site_1: XhoI; Site_2: EcoR; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 147 c 134 g 84 t
                                                  Location/Qualifiers
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/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
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bicolor cDNA,
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Best Local :
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                                                                                                                                                                                                                                                                          Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                        High quality sequence start: 3 High quality sequence stop: 481
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pcaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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BM318212
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PI1_79_G11.g9_A002 Pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An EST database from Sorghum; pathogen-induced plants
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/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42 of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves hirvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
the nathogen "The plant of the plant of the
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                               Location/Qualifiers
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Pred. No.
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/clone_lib="Pathogen induced 1 (PI1)" /note="Organ: Anthracnose-infected leaves from

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Query Match
Best Local
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76; Conser
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Cordonnier Pratt, M. - M., Gingle, A., Marsala, C. and P. An EST database from Sorghum: light-grown seedlings
                                                                                                                                                                                                                                                                                                              High quality sequence start: High quality sequence stop: !
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Fax: 706 583 0210
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/clone_Tlopt Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
: The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
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153 c
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Pred. No.
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Pred. No. 0;
Mismatches
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RESULT 12 AW672196

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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
Laboratory for Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The University of Georgia, 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE600412
PI1_96_A
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1 (bases 1 to 566)

Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Sciences Bu
Tel: 706 542 1860
Fax: 706 583 0210
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                             153
                                                                                                    /organism="Sorghum bicolor"
//db xref="taxon:4558"
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                                                                                 no effort was made to eliminate ESTs deriving from
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Pred. No.
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Query Match
Best Local S
Matches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCAGTACAGCGCCA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 570)
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PI1_71_G06.g1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 37 High quality sequence stop: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE597297.1 GI:9852370
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     Conservative
                                                                                                             /organism="Sorghum bicolor"
//db_xref="taxon:4558"
//clone_jlb="Pathogen induced 1 (PII)"
//clone_jlb="Pathogen induced 1 (PII)"
//clone_jlb="Pathogen induced 1 (PII)"
//note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation:
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."
                                                                                                                          Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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5.6%; Score 76; DB
100.0%; Pred. No. 0;
tive 0; Mismatches
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817 CGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTG 876

Query Match Best Local : Matches

th 5.6%; Standarity 100.0%; I Similarity 100.0%; I 76; Conservative 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE367035 575 bp mRNA linear EST 20-JUL-2000 PI1_42_B10.g2_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: High quality sequence stop: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                 142
                                                                                                                                         /organism="Sorghum bicolor"
//db_xref="taxon:458"
//clone_lib="Pathogen induced 1 (PII)"
//note="Organ: Anthracnose-infected leaves from localation;
two-week-old sorghum plants (ABTX 623
cultivar) were infected with pathogen (isolate FRM421 of Colletorrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (4 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. MARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."
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                        Score 76;
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Mismatches
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Search completed: May 3, 2003, 11:27:31 Job time : 1465 secs

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Oryza sativa perox
Herbicidally activ
Pinus radiata pero
Oryza sativa perox
Pinus radiata pero
Stylosanthes humil
Oryza sativa perox
Herbicidally activ
Oryza sativa perox
Eucalyptus grandis
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
725	725	725	727.5	727.5	728.5	739.5	739.5	739.5	753.5	755.5	765.5	771.5	774	774	778	799	801	801	801	801	808	813	813.5	818	822	846	863.5	863.5	866.5	866.5	867.5	870.5	870.5	885.5
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21	23	21	19	19	21	21	23	21	23	21	23	21	23	21	21	21	23	21	21	23	23	22	23	23	20	21	21	21	21	21	21 .	23	21	22
AAG17362	ABB93549	AAG17363	AAW44931	AAW73138	AAG08810	AAG41500	ABB93970	AAG41501	ABB93373	AAG44142	ABB93372	AAG06647	ABB91786	AAG30617	AAG08809	AAB16435	ABB91787	AAG43122	AAG21316	ABB91000	ABB93263	AAB99742	ABB91001	ABB78992	AAW87893	AAB16442	AAG14575	AAG14576	AAG49112	AAG49113	AAG14574	ABB93866	911	AAB99744
Arabidopsis thalia	11y	psis 1	eed	α		_	ч		~	s	⋖	G,	<		Arabidopsis thalia	Pinus radiata pero	~	Arabidopsis thalia					Herbicidally activ		Per5 roc	đ	is		Arabidopsis thalia		Arabidopsis thalia		4	Oryza sativa perox

ALIGNMENTS

RESULT 1 AAB99738

AAB99738 standard;

Protein;

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ААВ99738;

Ohashi Y, WPI; 2001-381695/40. N-PSDB; AAH44077. 08-DEC-2000; 2000WO-JP08728 Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grisea. Oryza sativa peroxidase s4235 protein SEQ ID NO:14. (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES 10-DEC-1999; 14-JUN-2001. WO200142475-A1 12-SEP-2001 Mitsuhara I, (first entry) 99JP-0352472 Sasaki T, Nagamura Y, Ito Ή Iwai T;

New set of rice peroxidase genes in rice under varying conditions

for

analysis of peroxidase expression production of rice plants with

```
The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CI given in Ani44071 to Ani44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the Peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea. CC The present sequence represents a rice peroxidase encoded by a gene from CC the gene set described above.
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Best Local
28-AUG-2001; 2001WO-EP09892.
                                     07-FEB-2002
                                                                         W0200210210-A2
                                                                                                                                                   Herbicidal;
                                                                                                                                                                                         Herbicidally active polypeptide SEQ ID NO 2570.
                                                                                                                                                                                                                                                                                                         ABB93359 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNLLGGPNWTVPLGRRDARTTSQSAANTNLPPPGASLASLLSMFSAKGLDARDLTALSGA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKAQLEASCKATVSCADIITLAARDA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                   plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                   agriculture;
                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                             324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 982.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                     herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5e-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
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WO200022099-A1

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RESULT 3
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                                                                                                                                                                             IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plants sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
                                                                                         Pinus radiata peroxidase protein sequence SEQ ID NO:389
                                                   Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
Pinus radiata; Monterey pine.
                                                                                                                        24-OCT-2000
                                                                                                                                                                             AAB16437 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 2570; 261pp + Sequence Listing; English.
                                                                                                                                                   AAB16437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as herbicides.
                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                             289
                                                                                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GYVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GASILRLFFHDCFVNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAVGLSTRDMVALSGAHTIGQSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                  GASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACP
                                                                                                                                                                                                                                                                                                                      APIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAM
                                                                                                                                                                                                                                                 IKMGDISPLTGSSGEIRKVCGRTN 324
                                                                                                                                                                                                                                                                           IRMGNVGVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                        APLDYTTAASFDNNYFKNLMTQRGLLHSDQVLFNGGSTDSIVRGYSNNPSSFNSDFTAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.1%;
61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 980; DB 23;
Pred. No. 6.1e-89;
6; Mismatches 77;
                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                   288
                                                                                                                                                                                                                                                                                                                                                                                                                                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
                                                                                                                                                                                                                                                                                                                                                               240
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Matches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 199; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2000
                                                                                                                                                                                                                                                                  Loca1
                                                                               CADILTIAARDSIVELQGPTWTVMLGRRDSTTASLSAANNNIPSPASSLSTLISSEQAHG
                                                                                                                                                                                                    CADILALAARDGTNLLGGGTTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQG
                                                                                                                                                                                                                                                                                                                               MQCLVAVSLLSC-----VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58
   SPLTGTNGQIRKNCRKSN 318
                                GVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                   VRLHFHDCFVNGCDGSILLDDNATFTGEKTAGPNANSARGFEVIDSIKTQVEAACSGVVS
                                                                                                                                                                                                                                                                                                                MRTLVCIGLMAVFVAFIHINAVNGQLSSTFYAKSCPRLPSIVKSVVKQAVAKEKRMGASL 60
                                                           TSITEDNKYYSNLKIQKGLLHSDQQLFNGGSTDSQVTAYSSNQNSFFIDFTAAMVKMGNI
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AA;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0169789.
99US-0143811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-NZ00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention.
                                                                                                                                                                                                                                                                                                                                                                                            60.2%;
                                                                                                                                                                                                                                                                                                                                                                             39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Score 965; DB 21;
Pred. No. 1.9e-87;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 318;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                           12;
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                                                                                           294
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AAB99741
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                                                                                                                                                                                                                    The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are given in AnH44071 to ANH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC detecting the component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea.

CC The present sequence represents a rice peroxidase encoded by a gene from the gene set described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BXXXX
                                                                                                                                                        Matches 189;
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohashi Y,
Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa; modification;
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB99741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB99741 standard; Protein; 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 174-176; 258pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAH44080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-381695/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000WO-JP08728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1999;
108
                              61
                                                           52
                                                                                                        QRMGASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEA 107
ACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLI 167
                              KRIGASIVRLFFHDCFVQGCDASLLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVET 120
                                                                                           MAQPTWSARRVTAALVVMVVVVLAVAGGSWAQLSPSFYSYSCPGVFNAVKRGMQSAIARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsuhara
                                                                                                                                                                                                                    327 AA;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase r3025 protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0352472
                                                                                                                                                                     59.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki T,
                                                                                                                                                      46; Mismatches
                                                                                                                                                   Score 954.5; DB 22;
Pred. No. 2.1e-86;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ħ
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Length 323; Indels

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CC encoding and representing the enzymes cinnamatte 4-hydroxylase (C4H), CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (ACL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, CC coniferol glucosyl transferase, caffeoyl CoA methyl transferase, CC coumerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenold hydroxylase, and isoflavone reductase, CC which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC content, composition and for producing a plant having altered lignin CC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any cryanism and for PCR amplification. The lignin content can be efficiently condified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; lignin;
Pinus radiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pinus radiata peroxidase protein sequence SEQ ID NO:395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 202-203; 213pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317962/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLFGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAMIRMGNVGVLTGTAGQIRRNCRVVN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Havukkala IJ
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99US-0143811.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16449 represent exemplification of
         plant cell transformed with Stylosanthes humilis Shpx6 peroxidase useful to confer on plants resistance to fungi, e.g. Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerotorium
                                                                                                                                                                                                                                                                         (RETR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxidase; Shpx6; transgenic plant; fungus resistance; disease protection; Phytophthora parasitica; Leptosphaeria maculans; Sclerotinia sclerotorium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW38217 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW38217;
                                                                                                                                    N-PSDB;
                                                                                                                                                             WPI; 1997-549739/50
                                                                                                                                                                                                                     Goulter KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TALSGAHTIGOARCTTFRGRIYGDTDINASFAALRQOTCPRS--GGDGNLAPIDVQTPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALSGGHTIGQAQCKNFRAHIYNETNIDSAYATSLRSKCPSTTGSGDSNLCPLDYMTPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAARDSVVELGGPSWTVMLGRRDSTTASKSGANSNIPPPTSSLSNLISLFQAQGLSAKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCFVNGCDGSVLLDDSSTITGEKTANPNANSARGFDVIDTIKSNVEKACSGVVSCADILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTSGQIPKNCRKPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGQIRRNCRVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDKNYYSDLKSQKGLLHSDQELFNGGSTDSQVTTYASNQNTFFSDFAAAMVKMGNIKPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDTAYFTNLLSRRGLEHSDQELFNGGSQDALVRQYSASASLENADFVAAMIRMGNVGVLT
                                                                                                                                 AAT95782
                                                                                                                                                                                                                                                                            COOP RES CENT TROPICAL PLANT PATHOLOGY GRAINS RES & DEV CORP.
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                                                                                                                                                                                                                     Kazan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humilis strain Paterson.
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                                                                                                                                                                                                                                                                                                                                                                      96AU-0009532.
                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-AU00253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide and protein sequences used in the present invention.
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Pred. No. 5.9e-86;
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Best Local Similarity 59.9
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance comprises introducing into cells of the plant a DNA construct comprising a promoter that is constitutively operative in the plant cell (preferably the cauliflower mosaic virus 355 promoter) and a Shpx6 DNA sequence (see AAT95782), or a hybridising sequence or fragment that encodes an enzyme with peroxidase activity. Also claimed are plant cells harboring the DNA construct, a plant comprising such cells, and material from such a plant, especially seed, politen, a stem segment or a cutting. Resistance to fungi, especially Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerotorium, can be conferred on cereal, legume, oilseed, sugar or fibre plants, particularly maize, banana, peanut, field pea, sunflower, tomato, canola, tobacco, wheat, barley, oat, potato, soybean, cotton,
                                                                                                                                                                                                           Oryza sativa peroxidase r2576 protein SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises the Shpx6 peroxidase of Stylosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 15-16; 30pp; English.
                                                                                                                                                           Oryza sativa; modification;
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                                08-DEC-2000; 2000WO-JP08728
                                                                14-JUN-2001
                                                                                               WO200142475-A1
                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                            AAB99746;
                                                                                                                                                                                                                                                                                                          AAB99746 standard; Protein; 314 AA
   10-DEC-1999;
                                                                                                                                                                                                                                          12-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVQGCDASVLLDDTSNFTGEKTARPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVA 128
                                                                                                                                                                                                                                                                                                                                                                                                                      AGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGYYKNLLVKKGLFHSDQQLFNGGSTDSQVNGYASNPSSFCSDFGNAMIKMGNISPLTGS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDSVVALGGPSWTVQLGRRDSTTASLSLANSDLAAPTLDLSGLISAFSKKGLSTSEMVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLIILVMSLIG-LGSGQLSSNFYATTCPNALSTIRSGVNSAVSKEARMGASLLRLHFHDC 68
                                                                                                                                                                                                                                                                                                                                                                                       SGQIRTNCRKTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A claimed method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 AA;
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                         rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 936.5; DB 18;
; Pred. No. 1.3e-84;
41; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineering a plant to fungal
ing into cells of the plant a
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CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene capression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the CC plants such as response to bacterial infection by Magnaporthe grisea.

CC The present sequence represents a rice peroxidase encoded by a gene from CC the gene set described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohashi Y,
Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a set of peroxidase genes found plants, especially rice, and their homologues, modified forms a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 205-207;
                                               set described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitsuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ito
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Query Match
Best Local Similarity
 Matches 185;
                                      Sequence
 Conservative
         57.78;
59.18;
 42;
Score 926; DB 22;
Pred. No. 1.4e-83;
12; Mismatches 82;
  82;
                  Length 314;
  Indels
  4;
 Gaps
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314 AA;

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122 AARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMT 181
                                   4
                                                                                                                     2 ASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL 61
                                                                                                     ASSVSLMLLVAAAMAS-AASAQLSATFYDTSCPNALSTIKSAVTAAVNSEPRMGASLVRL
                                          121
                                                                        121
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B δÃ

242 240 299

ALSGAHTIGQAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAF

241

QΥ

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182

300 TAGQIRRNCRVVN 312

Q

밁 302 TQGQIRLNCSKVN 314

RESULT 8 ABB93867 XXXXXXX 31-MAY-2002 ABB93867; ABB93867 standard; Protein; 325 (first entry)

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RESULT 9
AAB99743
ID AAB9
XX
AC AAB9
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 3078; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tjetjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP09892
  AAB99743;
                           AAB99743 standard; Protein; 326
                                                                                             316
                                                                                                                     303
                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                       136
                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                     10 LVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ 69
                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                  2002-269010/31
                                                                                                                                                                                                                                                       SVLLMGGRGWSVKLGRRDSITASFSTANSGVLPPPTSTLDNLINLFRANGLSPRDMVALS
                                                                                                                                                                                                                                                                      GTNLLGGPTWSVPLGRRDSTTASASLANSNP-PPPTASLGTLISLFGRQGLSPRDMTALS 184
                                                                                                                                                                                                                                                                                                                        GCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARD
                                                                                                                                                                                                                                                                                                                                                             YFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAG
                                                                                                                                                                                                                                                                                                          GCDASILLDDTRSFLGEKTAGPNNNSVRGYEVIDAIKSRVERLCPGVVSCADILAITARD
                                                                                            QIRRSCRRPN
                                                                                                                     QIRRNCRVVN 312
                                                                                                                                               YFMQLVNHRGLLTSDQVLFNGGSTDSIVVSYSRSVQAFYRDFVAAMIKMGDISPLTGSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              56.98;
                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 912.5; DB 23;
Pred. No. 3.2e-82;
""matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 3078
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                               135
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The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea. CC The present sequence represents a rice peroxidase encoded by a gene from CC the gene set described above.
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                              δÃ
                                                               Вр
                                                                                                                                                                                                                                                     Matches 170;
                                                                                                                                                                                                                                                                         Query Match
Best Local
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Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200142475-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with \cdot desired characteristics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2001
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 186-188; 258pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
   193
                                                                 133
                                   180
                                                                                                120
                                                                                                                              73
                                                                                                                                                                                            13
                                                                                                                                                              65
                                                                                                                                                                                                                          0
LAALSGAHTVGRASCVNFRTRVYCDANVSPAFASHQRQSCPASGGDAALAPLDSLTPDAF
                                                                                                                                                                                                               LMQCLVAVSL-LSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-381695/40
                                                                                ALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRD 179
                                                                                                                              DCFVGGCDASVLLDDTPAAPGEKGVGPNAVGSTTVFDLVDTIKAQVEAVCPATVSCADVL
                                                                                                                                                 DCFVQGCDGSILLD----AGGEKTAGPN-LNSVRGFEVIDTIKRNVEAACPGVVSCADIL 119
                                                                                                                                                                                           LLLLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYH 72
                    MTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRF
                                                                 AIAARDSVNLLGGPSWAVPLGRRDALSPSRSAVSTDLPGPEADISALVSAFAAKGLSSRD
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitsuhara
                                                                                                                                                                                                                                                                                                                         326 AA;
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase s10927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0352472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I,
                                                                                                                                                                                                                                                                           56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki T,
                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                          Score 901; DB 22;
Pred. No. 4.5e-81;
1; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagamura
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                                                                                                                                                                                                                                                                                           Length 326;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                               Gaps
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Matches

180;

46;

Mismatches

85;

5,

Gaps

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RESULT 10
AAB16426
ID AAB16
XX
XX
AAB16
XX
AAB16
XX
Plant
XW
Plant
XW
Plant
XW
Plant
XW
Pinus
OS Eucal
XX
PF
06-OC
XX
OS-OC
PR
14-JU
XX
PI Bloks
XX
PI Bloks
XX
PI Bloks
XX
PI Bloks
XX
OS-OC
PR
A (GENE
PA (FLET
XX
INOVEL
PT pathw
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STruc
XX
PT pathw
PT pathw
CC counda
CC (OMT)
CC COUNG
CC CUMD
CC Specific
CC Specific
CC Specific
CC Specific
CC Condific
CC Specific
CC Condific
CC CONDIC
C
                                                                                                                                                                                           The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-OcA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase; (CGT), coniferin beta-glucosidase (CBG), CC caffeic acid methyl transferase, caffeoyl CA methyl transferase, CC coumerate COA ligase (YSC), CC caffeic acid methyl transferase, caffeoyl CAA methyl transferase, flavenold hydroxylase, and isoflavone reductase, CC coumerate COA ligase, flavenold hydroxylase, and isoflavone reductase, CC councerate COA ligase, flavenold hydroxylase, and isoflavone reductase, CC which are involved in the lignin blosynthetic pathway. The CC polynucleotides can be used for modulating lignin content, lignin CC content, composition and the structure of a plant, especially eucalyptus and pine CC specially and for producing a plant having altered lignin CC content, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DAA and RNA sequences in any CC content, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DAA and RNA sequences in any CC content and CC productation. The lignin content can be efficiently condified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to CC AAB16449 represent polynucleotides and protein sequences used in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 193; 213pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317962/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis; Pinus radiata; Monterey pine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eucalyptus grandis peroxidase protein sequence SEQ ID NO:378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB16426 standard; Protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STGEVRLNCRKVNS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGQIRRNCRVVNS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIGYYRNIVAGAGILHSDQELFINGPVDSVVQLYSSNAAAFSSDFAASMIRIGNIGPLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0169789.
99US-0143811.
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                                                                                                                                                                               the present
56.1%;
57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
899.5; DB 2
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Query Match Best Local Similarity

Score Pred.

21;

Length 315;

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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AnH44071 to AnH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating NNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed
                                                                                                                                                 Disclosure; Page 192-194; 258pp;
                                                                                                                                                                               in rice
desired
                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000; 2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB99744 standard; Protein;
                                                                                                                                                                                                          New set
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DB; AAH44083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVGFSVVVVLLATSVIT-TARCKLSPSHYQSTCPKALSIVRAGVAKAIKNETRTGASLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VREDTAYETNILSRRGLEHSDQELENGGSQDALVRQYSASASLENADEVAAMIRMGNVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVALAARDSVVHLGGPSWTVSLGRKDSITASRSLANTSIPPPTSNLSALITSFAAQGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKGSNGQIRKNCRKVN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFFDNLYYHNLLQKKGLLHSDQELFNGSSVDSLVKKYACDTGKFFRDFAKAMIKMSEIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKNMVALSGSHT IGLARCTSFRRRIYNDSNIDTSFAHKLQKICPRIGNDSVLQRLDIQTP
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                                                                                                                                                                             of rice peroxidase genes
under varying conditions
characteristics
                                                                                                                                                                                                                                                                                                Mitsuhara
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infection; Magnaporthe grisea.
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Best Local :
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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
08-APR-1999
16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea. The present sequence represents a rice peroxidase encoded by a gene from the gene set described above.
                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                    EP1033405-A2
                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 62095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG49111 standard; Protein; 316 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGEIRLNCSRVN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAVSVLVVALAAAASGQLSTTFYASSCPTALSTIRSAVNAAVAREPRMGASLLRLHFHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDSVVALGGPSYPVELGRRDGMTTNQTMANTNLHPPTTDLGNFVTSFAGKGLSPTDLVV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFTDLIAGRGLLHSDQELYRGDGSGTDALVRVYAANPARFNADFAAAMVRMGAIRPLTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 55.2%; al Similarity 57.4%; 179; Conservative 4
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 990S-0121825

990S-0123180

990S-0125748

990S-0125786

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990S-0127462

990S-012834

990S-0128914
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Pred. No. 1.5e-79;
46; Mismatches 76
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promoter;
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     10-APR-1999

04-APX-1999

05-MAY-1999

06-MAY-1999

06-MAY-1999

07-MAY-1999

11-MAY-1999

14-MAY-1999

14-MAY-1999

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14-MAY-1999

19-MAY-1999

20-MAY-1999

21-MAY-1999

21-JUN-1999

21-JU
 14-JUN-1999
16-JUN-1999
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17-JUN-1999
18-JUN-1999
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23-APR-1999;
23-APR-1999;
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9908-0134941

9908-0135124

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990S-0131449

990S-013248

990S-0132484

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990S-0132486

990S-0132487

990S-0134256

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990S-0134218

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99US-0139763.
99US-0139817.
99US-0139899.
99US-0140353.
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99US-0145085.
99US-0145089.

99US-0145918. 99US-0145918. 99US-0145919.

04-AUG04-AUG05-AUG05-AUG06-AUG06-AUG06-AUG06-AUG09-AUG-

990S-0146386 990S-0146389 990S-0147038 990S-0147038 990S-0147202 990S-0147192 990S-0147303 990S-0147303 990S-0147416

10-AUG-11-AUG-12-AUG-13-AUG-13-AUG-16-AUG-17-AUG-

5-0149426. 5-0149722. 5-0149723. 5-0149929. 5-0149902. 5-0149930.

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RESULT 13
ABB93866
ID ABB93
AC ABB93
XX 31-MA
XX Herbi
XX Herbi
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XX WO20C
XX WO20C
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Matches 177; Conservative
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29 - CCT - 1999
28-AUG-2001; 2001WO-EP09892.
                                      07-FEB-2002.
                                                                       WO200210210-A2
                                                                                                           Arabidopsis thaliana.
                                                                                                                                              Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                  Herbicidally active polypeptide SEQ ID NO 3077.
                                                                                                                                                                                                                       31-MAY-2002
                                                                                                                                                                                                                                                                                              ABB93866 standard; Protein; 316
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                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 14489.
                                                                                                                                       AAG14574 standard;
          Arabidopsis thaliana
                                                                                              17-OCT-2000
                                                                                                                   AAG14574;
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	. ·		ID NO: 62097. pathway; metal expression con
			, netabolic pathway; control; promoter;
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188 TIGQARCTIFRGRIYGDIDINASFAALRQQTCPRSGGDGN--LAPIDVQTPVRFDTAYFT 245
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182 TIGRAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYK 241
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Search completed: April 26, 2003, 12:33:32 Job time: 78 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
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Listing first 45 summaries
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11: gb_htc:*
11: gb_hest3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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500.6	500.6	517 3	537.6	605.6	Score		
37.0	37.0	39.7	39.7	44.7	Match	Query	3
602	538	633	850	848	Match Length DB ID		
12	12	10	9	9	BB		
BG463106	BG842311	AW671673	AI374530	AA979912	ij		
BG463106 EM1_47_E1	AW672124 LG1_357_F BG842311 MEST29-D0	AW671673 LG1_349_F	AI374530 MEST3-D6	AA979912 MEST3-D6	Description	. •	_

45	44	43	42	41	40	9	38	37	36	ω	34	33	32	ω	3 0	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7
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342	6787	9936	5766	6287	1249	6518	6166	0407	8746	0016	4436	BE601026	445	0780	6346	36691	G64932	E59952	BE600529	E59436	E59746	G46319	E59553	E35755	E12530	93	E36622	E60011	67101	E60014	G84185	E35847	E36173	E59743	G46279	E36151	E36235	E3622(
503342 AL503342	F267871 HV CEAOC	599361 PI1 88 F	E357660 DG1 21 H	G462873 EM1 45 F	E412497 MCG003.F	F265184 HV_CEaOC	E361662 DG1_81_G	404079 WHE1201	W287460 LG1_228	E600167 PI	0744368 WHI	601026	324451 PIG	07804 76	263468 HV	366914 PI	549323 EM1 78	59526 PI1 8	500529 PI1_9	94365 PIL 3	597461 PI1 6	163190 EM1 4	595535 PI1 5	357554 DG1	125306 DG1_1	00823 PII	366224 PI1	600110 PI1	71012 LG1	600142 PII	41858 MEST	358471 DG1 30	E361738 DG1 82	97430 PI1 69	62797 EM1 4:	61528 DG1	62356 DG1 86	62200 DG1 85

ALIGNMENTS

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·	COMMENT	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AA979912
Schnable laboratory Iowa State University G405 Agronomy, Ames, IA 50011, USA Tel: (515)-294-0975 Fax: (515)-294-2999 Email: schnable@lastate.edu PCR PRimers FORWARD: twl412 (5'-GAAGATACCCCACCAAACC-3') BACKWARD: T7-VJ (5'-TAATACGACTCACTATAGGGC-3') Plate: MEST3 row: D column: 6 Seq primer: tw1412 (5'-GAAGATACCCCACCAAACC-3').	Contact: Schnable, PS	Expressed Sequence Tags from B73 Maize Seedlings	Wen, T.J., Ashlock, D.A. and Schnable, P.S.	1 (bases 1 to 848)	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Zea mays	Zea mays.		AA979912.1 GI:3157290	AA979912	.TW1412.Seq ISUM2 Zea mays		•

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    985 AACTGCCGGGTCGTCAACA
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                                                                                      GACGCGCTGGTGAAGCAATACAGCGCCCAGCGCCTNGCTCTTCAACGCCGACTT-GTGGCA
                                                                                                     GACGCGCTGGTGAGGCAGTACAGCGCCCAGCGCCTCGCTCTTCAACGCCCGACTTCGTGGCA 924
                                                                                                                                                            CTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGGTCGCAG 864
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                              ACCATGATTANGATGGG-AACCTTTGGGTGCTCAACCGGACCGTTGG-NAGATCAAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/cultivar="B73"
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95.78;
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GTGAACCCCTTTCGCGGNNGGNAATTTATGNGACCNAAACATNAACGCCTCCCTTCTNGG
                                                                                                                                                                                                                            TGCACCACCTTCCGCGGCC-GCATCTACGGCGACACCGACATCAACGCCT-CCTTCGCGG 703
                                                                                                                CTGTCGCCGCG----GACATGACGGCGCGTGTCGGGCAGCGCACACCATCGGGCAGGCCCGG 645
                                                                                        CTNTCCCCCCCCCGAAAANTAAGGCGCTNTCGGGGGCGNACACNNATGGGCAGGGCCGG
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MEST3-D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G405 Agronomy, Ames, IA 50011, Tel: (515)-294-0975 Fax: (515)-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')

Plate: MEST3 row: D column: 6

Seq primer: POLYT-N (5'-TYTTTTTTTTTTTTTTTTTTTTTTT(AGC)-3').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
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Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
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BACKWARD: T7-YJ (5'-TAATACGACTCACTATACCCC-3
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                                                                                                                                                                                                                                                                                                                                                                                 follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNASE H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."

226 c 210 g 194 t 52 others
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ECORI; Site_2: XhOI; ds-CDNA molecules were generated as
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/dev_stage="Two-leaf-stage green se
/lab_host="XL1-MFR Blue"
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/db_xref="taxon:4577"
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Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Por
Clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 633)
1 (bases 1 to 633)
                                                                                                                                                                                                                                                                                                                     sequence.
AW671673
                       Seq primer: JEN REV High quality sequence POLYA=No.
                                                                      Email: mmpratt@uga.edu
Sequences have been tri
below Phred quality 16
                                                                                                                                Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                    Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. An EST database from Sorghum: light-grown sees Unpublished (2000)
Contact: Cordonnier-Pratt MM
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LG1_349_F09.b1_A002 Light
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706 583 0210
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aceae; PACC;
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AW672124
AW672124.1
Sorghum bicolor
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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LG1_357_F02.b1_A002 Light
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GI:7536032

625 bp t Grown ᆫ

mRNA (LG1)

Sorghum

linear EST 19-JUL-2000 ghum bicolor cDNA, mRNA

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                                                                                  GCCCTGTCCGGCCCCCACACCATCGGGCAGCCCGGTGCACCACCTTCCGCGGCCGCAT
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/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
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2.3e-71;
hes 55;
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                                                                           AACGTGCCGCTGGGCCGGGGACTCGACGACGGCAAGCGCGTCCCTTGCCAACAGCAAC
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, US/
Tel: 706 542 1860
Fax: 706 583 0210
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High quality sequent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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/clone_lib="flight Grown 1 (LG1)"
/clone_lib="flight Grown 1 (LG1)"
/note="organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
233 c 188 g 110 t 2 others
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BG842311
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VERSION
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                                                                       677 ACACCGACATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGTGCCCGCGGGTCCGGGC 736
 61
                                                          1 ACACCGACATCAACGCCTCCTTCGCGGCGCGCGCGCGCAGCAGACGTGCCCGCGGTCCGGCG
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BG842311.2
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Zea mays
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G405 Agronomy, Iowa State University,
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On May 25, 2001 this sequence version replaced g1:14208633
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 538)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
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MEST29-D08.T3
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pcaceae; PACC
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                                                                                                                                                                                           121
                                                                                                                  Conservative
                                                                                                                                                                                     schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST29-D08"
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
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                                                                                                                                Score 500.6; DB 1
Pred. No. 7.2e-66;
                                                                                                                     Mismatches
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91.3%;

Pred.

No.

6.8e-66;

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BG463106
BG463106.1
                                                                                                                  High qual POLYA=No.
                                                                                                                                                     Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA ?
                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
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Reid, S.P., Cordonnier-Pratt, M.-M.,
An EST database from Sorghum: deve
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EM1_47_E12.b1_A002
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706 583 0210
    /clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
a 219 c 192 g 90 t
                                                                         /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                        Location/Qualifiers
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                                                                                                                          sequence stop:
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Sorghum bicolor
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for highest quality
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30602-7271,
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CDNA, mRNA
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Query Match

37.0%;

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Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trim
below Phred quality 16
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                                                                                         Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
                                                                                                                                                                                         clade; Panicoideae; Andropogoneae; 1 (bases 1 to 593)
Cordonnier-Pratt, M.-M., Gingle, A.,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoidae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                          sorghum.
Sorghum bicolor
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DG1_85_C06.b1_A002 Dark Grown
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BE362356
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EST.
sorghum.
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
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/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: Dark-grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector: 1 (DG1)"
/note: 5-day-old
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Sequences have been trimmed
below Phred quality 16. The
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Fax: 706 583 0210
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The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
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Unpublished (2000)
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryoph/ta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG462797
EM1_45_F11.b1_A002 Embryo
                                                                                                                                                                                                                                                                                                                       High quality
                                                                                                                                                                                                                                                                                                                                  Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                            Sequences have been below Phred quality
                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sorghum.
                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 591)
                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.P., Cordonnier-Pratt, M.-M.,
                                                                                   Conservative
                                                                                                                                                /Clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector: Note: Steel: 1: Not: Site_2: EcoR; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

214 c 190 g 87 t
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/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                               36.2%;
91.1%;
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                                                                                  Score 489.6; DB Pred. No. 3e-64; 0; Mismatches
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bicolor
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RESULT 11
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Seq
                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                   An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                BE597430 589
PI1_69_D10.b1_A002 Pathogen :
                                                                                         High quality sequence POLYA=No.
                                                                                                                                                                                                                                                                                         Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                  clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                  primer: JEN REV
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706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leave
two-week-old sorghum plants 48 hr after
                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                          Location/Qualifiers
                                                                                                   stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                9 bp m
                                                                                                                                          to exclude PolyA, vector and regions threshold for highest quality sequen
                                                                                                                                                                                                                                                                   pathogen-induced
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1 1 (PI1) Sorghum bicolor cDNA,
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BE361738
BE361738.1
EST.
 Sorghum
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DG1_82_H08.b1_A002
              sorghum
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bicolor

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Dark

Grown

) _p

mRNA (DG1) Sc

NA linear EST 20-JUL-2000 Sorghum bicolor cDNA, mRNA

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ACCTGAACTCGGTGCGCGCGTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGGCCG
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                                                                                TCAGCAATGACCAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: ECORI; Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (Isolate FRM42I of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings (2 weeks old) exhibit juvenile registant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
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87.5%;
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COMMENT

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                                                                                                                                                                                                                                T.H.
An EST database from Sorghum: dark-grown Seedling.
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is 20.
Seq primer: JEN REV
High quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 561)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/clones_to_be sequenced were prepared by mass excision."
a 195 c 166 g 106 t
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Pred. No. 3.6e-57;
D; M1smatches 56;
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AUTHORS
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Best Local Sim
Matches 484;
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                                                                                                                                                                                                                                                                                          TCATTCACCGAGCGTGCAGGCAGGCAGCAGCTTGCCCATGGCGTCTCCCACCTTGATGC 88
                                                                                                                                             TTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAGAAGACCGCCGGGCCGA 328
                                                                                                                                                                                                                                  TCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCCAATTCGGCGCGCGCTTTGAGGTCATCGACACCATCAAGACCAACGTGGAGGCCG
                                                            ACCTGAACTCGGTGCGCGCGTTTGAGGTCATCGACCATCAAGCGGAACGTCGAGGCCG
                                                                                                                       TCAGCAATGACCAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
1 (bases 1 to 570)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE358471 570;

DG1_30_A01.bl_A002 Dark Grown

sequence

BE358471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE358471.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="bark Grown 1 (DG1)"
/clone_llb="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/notea Torgan: 5-day-old dark-grown seedlings; Vector: 5-day-old dark-grown seedlings; Vector: 5-day-old dark-grown seedlings; Vector: 5-day-old dark-grown seedlings; Vector: 
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1. .570
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Pred. No. 4.1e-57;
0; Mismatches 70;
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BG841858/c
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497
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BG841858
BG841858.2
EST.
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FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 446)
(du.F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)

On May 25, 2001 this sequence version replaced gi:14208180.

Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG841858 446 bp mRNA linear E MEST27-D09.T3 ISUM4-TN Zea mays cDNA clone MEST27-D09
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                                                                                                   /tissue_type="Seedling and silk"
//lab_host="DHIDB"
                                                                                                                 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_"MEST27-D09"
/clone_lib="ISUM4-TN"
                32.5%;
                Score 439.6; DB 12; Pred. No. 1.1e-56;
                                    Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 29-MAY-2001
)9 3', mRNA
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SOURCE
ORGANISM
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AUTHORS
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VERSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 564)
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum: pathogen-induced plants (Inpublished (2000))
Contact: Cordonnier Pratt MM
Laboratory for Genomics and Bioinformatics
Laboratory for Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
is 20.
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564 bp mRNA linear EST 18-AUG-2000
PRIL_79_G11.bl_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
                                                                                                                                                                                     Seq primer: JEN REV
High quality sequence stop:
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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BE600142
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from two-week-old sorghum plants 48 hr after inoculations."
                                                                                                                                                              Location/Qualifiers
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for highest quality sequence
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27 619 87 559 207 439 267 379 327

vector and

USA

inoculation;

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BASE COUNT
ORIGIN
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                                                   569 CCCTGTTC 576
                                                                                                 497 GCGCGTCCCTTGCCAACAGCAACCTCCCGCAGTCGACGGGGAGCCTGGGTACGCTCATCT 556
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US-09-938-842A-783
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US-09-938-842A-1719
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sequence 11, Appl sequence 254, Appl sequence 1711, Appl sequence 1632, Appl sequence 11632, Appl sequence 2559, Appl sequence 2693, Appl sequence 2693, Appl sequence 1714, Appl sequence 1714, Appl sequence 1714, Appl sequence 1718, Appl sequence 1518, Appl sequence 1719, Appl sequence 1719, Appl sequence 1773, Appl sequence 1774, Appl sequence
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Sequence 2181, Ap	Sequence 2570, Ap	Sequence 2630, Ap	Sequence 2656, Ap	Sequence 50, Appl	Sequence 2184, Ap	Sequence 1596, Ap	Sequence 3718, Ap	Sequence 682, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 989, App	Sequence 1457, Ap	Sequence 858, App	Sequence 1498, Ap	Sequence 2727, Ap	•	•		•		Sequence 217, App			Sequence 166, App

ALIGNMENTS

US-09-938-842A-60

GENERAL INFORMATION:

Sequence 60, Application US/09938842A Patent No. US20020160378A1

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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 60
LENGTH: 1017
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Matches 485; Conservative
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
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                                       144 CGAGGAGATCGTGAGGTCAGTTGTAGCCAAAGCTGTTGCAAGGGAGACTCGTATGGCTGC
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APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Defense-Inducible Ge:
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT FILING DATE: 2011-10-23
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                         US-10-027-559-11
                                                                                                                                                                     Sequence 11, Application US/10027559 Patent No. US20020144307A1 GENERAL INFORMATION:
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TYPE: DNA
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; FEATURE:
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; LOCATION: (0)...(0)
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; LOCATION: (18)...(1088)
US-10-027-559-11
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Best Local Similarity 52.8
Matches 491; Conservative
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Pred. No. 2.2e-36;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Pred. No. 3.
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SOFTWARE: PatentIn v. SEQ ID NO 83; LENGTH: 824; TYPE: DNA TYPE: DNA ORGANISM: Zea mays
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Best Local Similarity
Matches 425; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 83, Application US/09894633A Patent No. US20020124285A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MASUCCI, JAMES
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPREFILE REFERENCE: 38-21(15856)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/894,633 PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Conner, Timothy
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                                                                                                              CTTCTCGACGCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAA-----
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PRIOR PLICATION NUMBER: US 60/264,647
PRIOR ETLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1711
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                      ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1711
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: Sequence 1711, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
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                                                                     Query Match
Best Local
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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                                                                     Similarity
                                                       Conservative
                                                                    11.1%;
                                                  Score 150; DB 9; Lo
Pred. No. 2e-30;
0; Mismatches 435;
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong

T: Wang, Xun
T: Zhu, Tong
INVENTION: STRESS-REGULATED

GENES

OF PLANTS,

TRANSGENIC

PLANTS CONTAINING

RESULT 6 US-09-938-842A-1632

Sequence 1632, Application Patent No. US20020160378A1

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TTGACAGGTTCTAGTGGCGAAATCAGGAAGATTGCAGGAAGATTAAC
                                                                       GCCTCGCTCTTCAACGCCGACTTCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTG
                                                                                                               CAAGTTCTGTTCAGCAGTAACGAGAAATCGAGAGGAGCTTGTGAAGAAGTATGCAGAAGAT
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                                                         CAAGGAGAGTTTTTTGAGCAATTTGCGGAAATCGATGATCAAGATGGGAAATATCTCTCCC
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FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2000-08-24

PRIOR PPLICATION NUMBER: US 60/264,647

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-29

PRIOR PILING DATE: 2001-05-22

RUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1632

LENGTH: 1041
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                                                                                                                                 CTAAAGGACACGTGTCCTAACGTGGACTCCTCAGACTCTAAGCTCGCTGCTCTTGACGCA 801
                                                                                                                                                                   CAGACGTGCCCGCGGTCCGGCGGCGACGGC------AACCTGGCGCCCCATCGACGTG 765
                                                                                                                                                                                                                            TTCCGCGGCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCGCGGCGCGCTGCGGCAG 714
                                                                                                                                                                                                                                                                                            GAGAATATAACAGCCAAGTTCGTGACCCTTGGACTCGACCTCAAGGACGTTGTTGTCCTC 621
                                                                                                                                                                                                                                                                                                                                                                                                           TCATTAACGGCGAGTGAGCAAGCGGCGAATACAAATCTGCCATCTCCGTTTGAGGCGTTG
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TTGGATTCTGATCAAACCCTAATGACAGATCCTACGGCTGCCGCCTTGGTGAAGTCGTAC
                                TTCCACTCGGACCAGGAGCTCTTCAACGGCGGCTCGCAGGACGCGCTGGTGAGGCAGTAC 885
                                                                GCTAGCTCAGTCAAGTTTGACAATGCTTACTACGTGAACTTAATGAACAACATAGGACTG
                                                                                                                                                                                                     TTCAAGGGCTCAGGCCAGCCTGACCCAAACCTAGCCGCTTCCTCAGCACTTCTCTAAG
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CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 1167
LENGTH: 251
TYPE: DNA
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158231H1
US-09-923-876-1167
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GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tony
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                    Sequence 2559, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.3
Matches 180; Conservative
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
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CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24

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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kemigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FRO)
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-66
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-25
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 3446
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PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2559
SEQ ID NO 2559
LENGTH: 1011
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Sequence 3446, Application US/09923876; Patent No. US20020013958A1; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2559
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TYPE: DNA
                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 GATCCTAGAAATGCAGCCATAATTATTCGTCTTCACTTCCACGACTGCTTTGTCCAAGGA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 TCCGAATGTCCTGGAGTTGTTTCATGCGCTGATCTTCTCACAATTGGTGCTAGAGATGCT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACACGATCGGAAAAGCACAATGTCGCAACTTCCGATCCCGAATTTATGGAGA 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGATGGATCGGTGTTGCTAGACGAGACAGAAACTCTACAGGGAGAGAAGAAAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACACCATCGGGCAGGCCGGTGCACCACCTTCCGCGGCCGCATCTACGGCGA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAGCGCCTCGCCCAACAGCAACCCCCCCCCCCGACGGCCAGCCTCGGCACGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAACCTTCTCGGCGGGCCGACCTGGAGCGTGCCGCTCGGGCGGCGGGACTCGACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGCTAAGTTCTATTCTCAAGGTCTCTCGGTTGAAGACATGGTCGCTCTTATAGGAGCG
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700162281H1
US-09-923-876-3446
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; ORGANISM: Arabidopsis thaliana
.US-09-938-842A-2693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2693
LENGTH: 993
                                                                                                                                                                                                                                                                                                                Matches 439;
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-66-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                                     128 ACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574
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                                                                                                              146 AGCAGGCGGTTACTACAAAATTCAAACAAACTGTCACAACGGCTCCTGCAACGTTGCGGA 205
  266
                                      298 --GACGCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGG 355
                                                                                                                                                                                           188 GGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTCAGGC 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                  86 ATGCTCAACTGTCAGAGAATTACTACGCCTCGACATGTCCTAGCGTAGAGCTCATCGTTA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGGCAGGCAGGCCTGTCGCCGCGCGACATGACGGCGCGCTGTCGGGCGCGCACACCATC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCAAGCACGCTGCACCAACTTCAGAGCGCACGTGTAC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCAGGCCCGGTGCACCACCTTCCGCGGCCGCATCTAC 672
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ATGAAGACGCAGAGAAAGACGCAGATGACAATAAATCTCTCGCCGGAGACGGATTTGACA 325
                                                                           TGTTCTTTCACGACTGCTTCGTCGAGGGATGTGATGCGTCTGTGTTTATAGCATCTGAGA 265
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; Pred. No. 1.26
0; Mismatches
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Pred. No. 3.7e-22
                                                                                                                                                                                                                                                                                                                Mismatches 436;
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l.2e-21;
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APPLICANT: HATPER, Jeff
APPLICANT: HATPER, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: AND, Tong
APPLICANT: AND, Tong
APPLICANT: AND, TONG
APPLICANTON: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRLIDI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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US-09-938-842A-1980
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                                                                                                                                                                                                                                                                                             Sequence 1980, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1980
LENGTH: 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGCTAGGGAGACGAGACGGGCTCGTGTCGAAAGCGTCTAGAGTGACCGGCAAGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                990
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48.3%; Pred. No. 2.7e-21;
7ative 0; Mismatches 443;
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRITTLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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Local Similarity 48.1%;
ses 455; Conservative
GCCGCATCTACGGCGACACCCGACATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGT
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                                                            CGCATACGTTCGGGCGTGCTCGATGTGGAGTATTCAACAACAGACTATTTAACTTCAGCG
                                                                                                    CGCACACCATCGGGCAGGCCCGGTG-----
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: STRESS-REGULATED GENES OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2367
LENGTH: 942
TYPE: DNA
GRGANISM: Arabidopsis thaliana
US-09-938-842A-2367
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.; Sequence 2367, Application US/09938842A
; Patent No. USECONDIA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                           140 CGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGGCGATGA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 ACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAAAGACCG
                                                                                                                                                                                                         134 GCCAACGGTTTGGTGTTACCCCAACCGTTACCGCCGCTTTGCTCCGTATGCATTTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                14 CCAAGTTTTCATCTTCTTGTGCCTTTTCTTTATTTTTCCGATCGCATTTGCTCAACTGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 CCTTGATGCAATGCCTGGTCGCCGTTTTCCCTCTCTCTGTGTCGCCCACGACAGCTCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 437; Conserv
                                                                                                                                                                                                                                     CTGCTGGACCAAACGGAAGCGTCAGGGAATTTGACCTGATAGACCGGATCAAGGCTCAGC
                                                  CCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACG
                                                                                                                                                                                                                                                                                                              GAGTCGGGTTTTATAGTCAATCATGCCCTCAAGCCGAGACTATCGTACGCAATCTGGTGC
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                                                                                                    ACTGTTTCGTTAAGGGCTGTGACGCTTCTCCTCATTGATTCAACCAATTCCGAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 114; DB 9; Length 942;
46.9%; Pred. No. 9.8e-21;
ative 0; Mismatches 480; Indels
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GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRAITILE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR TILING DATE: 2001-01-16
PRIOR TILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 783
LENGTH: 981
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US-09-938-842A-783
; Sequence 783, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US20020160378A1
ORGANISM: Arabidopsis thaliana -09-938-842A-783
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'; TYPE: DNA; ORGANISM: Arabidopsis thaliana US-09-938-842A-1518
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                                                                                  NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1518
LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1518, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                     APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILLE REPERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2001-01-01
PRIOR PILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-05-22
PRIOR FILING DATE: 2001-06-22
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Best Local
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AMACCGTCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 CGGCCGCATCTAC 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 CCACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 CCAAGCTCAATTGCAGATGAATTTCTATGCCAATTCTTGTCCTAATGCTGAAAAGATTGT
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8.1%;
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Score 110;
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DB
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Length 987
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                                                                                                                                                                                                                                                                                                                                                                  564 CATCTCCCTGTTCGGCAGGCAGGCCTCTCGCCGCGGCACATGACGCGCGCTGTCGGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AGTCATTCTCACTCAAGGAACAGGCTGGCAAGTACCAACGGGACGTAGAGATGGTAGAGT 470
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                                                                                                                                                                                                                                                                                                   885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 TGTCCAAGGTTGTGACGGTTCGATCCTTATATCCGGAGCTAACACCGAGAGAACCGCCGG
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                                                828 TTGGACCGATCCAGCCACTAGACCCATAGTGCAACAATTGATGGCTCCTAGAAGCACCTT 887
                                                                                                                        846
                                                                                                                                                 768
                                                                                                                                                                786 CACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGCT 845
                                                                                                                                                                                                   708
                                                                                                                                                                                                                          726
                                                                                                                                                                                                                                                 648 ACAAACCGCAGATCCAACCATCGACCCAACATTTTTGGCGCAGCTTCAAACACAATGTCC
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                                                                                                                                                 CCAAAACGGCGACGGTTCAGTGCGCGTGGATCTCGACACCGGAAGCGGAAGCACTTGGGA
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                                                                                                                        CTTCAACGGCGGGTCGCAGGACGCGCTGGTGAGGCASTACAGCGCCAGCGCCTCGCTCTT 905
                                                                                                                                                                                                                       GCGGTCCGGCGACGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGA 785
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Search completed: May 3, 2003, 10:14:37 Job time: 137 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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1604
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-615-192A-389
US-09-615-192A-397
US-09-615-192A-394
US-09-615-192A-394
US-09-615-192A-397
US-09-615-192A-397
US-09-615-192A-397
US-09-615-192A-397
US-08-671-320-13
US-08-686-577-11
US-08-686-577-11
US-08-686-577-12
US-08-686-577-17
US-08-686-577-17
US-08-686-577-17
US-08-686-577-19
US-08-615-192A-388
US-09-615-192A-388
US-09-615-192A-386
US-09-615-192A-386
US-09-615-192A-385
US-09-615-192A-386
US-09-615-192A-386
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US-09-615-192A-387
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  Sequence 389, App Sequence 378, App Sequence 378, App Sequence 2, Appli Sequence 387, App Sequence 2, Appli Sequence 397, App Sequence 397, App Sequence 13, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 17, Appl Sequence 37, Appl Sequence 388, App Sequence 386, App Sequence 381, App Sequence 381, App Sequence 381, App Sequence 385, App Sequence 332, App Sequence 332
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US-09-615-192A-389
; Sequence 389, Application US/09615192A
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33.5 20.8 20.4 4 US-09-615-192A-390 30.5 19.0 95 4 US-09-615-192A-390 294.5 18.4 18.4 US-09-615-192A-390 294.5 18.1 12.0 4 US-09-615-192A-394 291 18.1 12.0 4 US-09-615-192A-393 289 18.0 111 4 US-09-615-192A-393 285 14.7 1114 4 US-09-615-192A-347 235 14.7 114 4 US-09-615-192A-347 231 13.8 103 4 US-09-615-192A-398 198.5 12.4 11.7 4 US-09-615-192A-398 198.5 13.4 11.7 4 US-09-615-192A-398 198.5 13.4 11.7 4 US-09-596-824-6 119.5 7.5 389 4 US-09-596-824-4 119.5 6.8 345 1 US-07-792-259-12 108.5 6.8 345 1 US-07-792-259-17	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
120 4 120 4 138 4 110 4 111 4 111 4 111 4 111 4 110 3 110 3	108.5	108.5	108.5	112	119.5	132.5	176.5	176.5	198.5	221	235	252.5	289	291	294.5	305	320	333.5
LL44440H4444444	6.8	6.8	6.8	7.0	7.5	8.3	11.0	11.0	12.4	13.8	14.7	15.7	18.0	18.1	18.4	19.0	20.0	20.8
4 US-09-615-192A-390 4 US-09-615-192A-390 4 US-09-615-192A-390 4 US-09-615-192A-394 4 US-09-615-192A-393 4 US-09-615-192A-333 4 US-09-615-192A-347 7 US-09-615-192A-398 4 US-09-615-192A-398 4 US-09-615-192A-398 6 US-09-615-192A-398 6 US-09-615-192A-398 7 US-09-615-192A-398 7 US-09-615-192A-398 8 US-09-615-192A-398 1 US-09-615-192A-398 1 US-09-615-192A-398 1 US-09-615-192A-398 1 US-09-596-824-4 1 US-09-596-824-4 1 US-09-596-824-4 1 US-09-596-824-4 1 US-09-596-824-4 1 US-09-596-824-4 1 US-09-792-259-12	364	345	344	366	389	362	121	121	117	103	114	118	111	120	138	95	120	202
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	US-07-792-259-17	US-07-792-259-12	US-09-024-532-4	US-09-596-824-4	US-09-596-824-2	US-09-596-824-6	US-08-462-695-12	US-08-190-029A-12	US-09-615-192A-400	US-09-615-192A-398	US-09-615-192A-347	US-09-615-192A-333	US-09-615-192A-379	US-09-615-192A-393	US-09-615-192A-384	US-09-615-192A-390	US-09-615-192A-392	60-
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ALIGNMENTS

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241 TSITEDNKYYSNLKIQKGLLHSDQQLENGGSTDSQVTAYSSNQNSEFIDETAANYKMGNI 300	235 TPVREDTAYFTNILSRRGLEHSDQELENGGSQDALVRQYSASASLFNADFVAAMIRMGNV 294	175 LSPRDMTALSGAHTIGQARCTTERGRIYGDTDINASEAALKQQTCFKSGGJUNHAFIDVO 234 : : : : : : : :	121 CADILTIAARDSIVELQGPTWTVMLGRRDSTTASLSAANNNIPSPASSLSTLISSFQAHG 180	115 CADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGROG 174	61 VRLHFHDCFVNGCDGSILLDDNATFTGEKTAGPNANSARGFEVIDSIKTQVEAACSGVVS 120	59 LRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVS 114	1 MRTLVCIGLMAVFVAFIHINAVNGQLSSTFYAKSCPRLPSIVKSVVKQAVAKEKRMGASL 60	7 MQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58	Query Match 60.2%; Score 965; DB 4; Length 318; Best Local Similarity 60.1%; Pred. No. 2.4e-95; Matches 191; Conservative 39; Mismatches 76; Indels 12; Gaps		TYPE: PRT ORGANISM: Pinus radiata	LENGTH: 318	SOFTWARE: FastSEQ for Windows Version 3.0	R OF SEQ ID NOS: 405	PRIOR APPLICATION NUMBER: US U9/109,/09		PRIOR APPLICATION NUMBER: US 08/713,000	RIOR APPLICATION NUMBER: US 08/975,316	CURRENT FILING DATE: 2000-07-12	FILE REFERENCE: 11000.1003c4U	ion of Plant Ligr	ANT:	APPLICANT: Bloksberg, Leonard N.	GENERAL INFORMATION:	Sequence 389, Application US/U9613132A Patent No. 6410718

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295 GVLTGTAGQIRRNCRVVN 312

SPLTGTNGQIRKNCRKSN 318

US-09-615-192A-395

Patent No. 64107 Sequence 395,

Application US/09615192A

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RESULT 3
US-09-615-192A-378
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GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant
FILE REFERENCE: 11000.1003cd.
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                                              Sequence 378, Application US/09615192A Patent No. 6410718
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Best Local
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PRIOR EILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR EILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
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                                                                                                                                                                                                                                                                             310 GTSGQIPKNCRKPN 323
                                                                                                                                                                                                                                                                                                                 299 GTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                    250 FDKNYYSDLKSQKGLLHSDQELFNGGSTDSQVTTYASNQNTFFSDFAAAMVKMGNIKPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 IAARDSVVELGGPSWTVMLGRRDSTTASKSGANSNIPPPTSSLSNLISLFQAQGLSAKEM
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; Pred. No. 1e-93;
44; Mismatches 74; Indels
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1 MASPTLMQCLVAVSLLSC--VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58

Query Match
Best Local Similarity
Matches 170; Conserv

Conservative

32;

Score 846; DB 4; Pred. No. 1.1e-82; 2; Mismatches 58

58;

6,

Gaps

2;

Length 266 Indels

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US-09-615-192A-394
                                                                                                                                  PRIOR FILING DATE: 199
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 394
LENGTH: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 394, Application US/09615192A Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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LENGTH: 315
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bloksberg, Leonas
APPLICANT: Havukkala, Ilkka
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
                                                                                          ORGANISM: Pinus radiata
                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 DIVALAARDSVVHLGGPSWTVSLGRKDSITASRSLANTSIPPPTSNLSALITSFAAQGLS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LFFHDCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVGFSVVVVLLATSVIT-TARCKLSPSHYQSTCPKALSIVRAGVAKAIKNETRTGASLLR
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                                                                                                                                                                                   for Windows Version 3.
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52.7%;
63.9%;
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Patent No.
                                                                                                                                          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: STUART, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEPHONE: 317 337 4816
TELEPHONE: 317 337 4817
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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                                                                                                                                 TOPOLOGY: 1:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DowElance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: I
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                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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TSMGCLVLLCLVSSLLPSAVLGHPWGGLFPQFYDHSCPKAKEIVQSIVAQAVAKETRMAA: 62
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3, 6384207
                                                                       Similarity
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Belmar, Scott
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                                                        51.2%; Score 822; DB 4;
51.1%; Pred. No. 5.8e-80;
tive 51; Mismatches 90;
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                                                                                     Length 333;
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; SOFTWARE: FastSEQ for Wir
; SEQ ID NO 387
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-615-192A-387
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APPLICANT: Havukkala, Ilka
APPLICANT: Havukkala, Ilka
APPLICANT: Havukkala, Ilka
ITILE OF INVENTION: Materials and Methods fo.
ITITLE OF INVENTION: Modification of Plant Li
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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Best Local Similarity
Matches 162; Conserv
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NUMBER OF SEQ ID NOS: 405
FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 QGLSPRDMTALSGAHTIGQARCTTFRGRIY------GDTDINASFAALRQQTCPRSGGD 225
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246
                                            239
                                                                                                                                                                                                      121 LAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPRDM 180
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                                                                                                                                181 TALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVR 238
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                                                                                                                                                                                                                                                                                                 DCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA 120
FDKNYYYNLKSKRGLLHSDQELFNGGSTDSHVTKYASNQNTF 287
                                                                                                                                                                                  IAARDSVVQLGGPSWKVMLGRRDSTTASISGANNNIPPPTSNLTKLISLFQAQGLSTKEM
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                                       FDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLF 280
                                                                                         VALSGGHTIGQAQCKNFRAHIYNDTNIDTTYATSLRSKCPSTTGSGDSNLSPLDYTTPTV 245
                                                                                                                                                                                                                                                                             DCFVNGCDGSVLLDNSTTFTSEKYALPNNNSARGFEVIDSIKSQLENACTGVVSCADILT 125
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RESULT 7
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local
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                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 397
LENGTH: 351
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APPLICANT: Desai, Nalini
ORGANISM: Pinus radiata -09-615-192A-397
                                                                                                                                                                                                                              FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11 PRIOR APPLICATION NUMBER: US 09/169,789
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U
                                                                                                                                             PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-10-09
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TYPE: PRT
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appLICANT: Havukkala, Ilkka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCDGSILLDTDGTQTEKDAAPNVGA-GGFDIVDDIKTALENVCPGVVSCADILSLASEIG
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Pred. No. 1.9e-68;
53; Mismatches 97;
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TYPE: PRT
; ORGANISM: Pinus radiata
us-09-615-192A-391
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Best Local Similarity
Matches 142; Conserv
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SEQ ID NO 391
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                                                                                                                                                                                   Matches
                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                               PRIOR FILING FOR THE PRIOR APPLICATION NUMBER: US OF THE PRIOR DATE: 1998-10-09
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                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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 121
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                                                             61
                                                                                           59
                                                                                                                                                                                   Match 38.9%; Sc
Local Similarity 64.7%; Pr
                                                                                                                      1 MASPTLMQCLVAVSLL--SCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNCRV. 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRLYNSTTGTOMRDPTMDQSFAKNLYLTCPTS-TTVNTTKLDIRTPNVFDNKYYVDLLNR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRIYG-----DTDINASFAALROOTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRRDSLTFANRSTVLANLPSPTSNVTGLISVLGPKGLNFTDLVALSGGHTIGRSNCSSFD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRRDSTT-ASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQARCTTFR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEQTAPPNLSLRAQALKIINDIKENVEAACSGIVSCADIVTLAARDSVVMAGGPFYPLPL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEKTAGPNIN-SVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNILLGGPTWSVPL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQG 174
                                                           LRLFFHDCFVQGCDGSTLLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVS 114
                                                                                                                                                                                                                                                                                                                         FastSEQ
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47.0%; Pred. No. 5.7e-63;
tive 55; Mismatches 93
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Pred. No. 4.8e-59;
1; Mismatches 44
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US-08-671-320-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-998-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO. 103RD STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                    292 GNVGVLTGTAGQIRRNCRVVNS 313
                                                                                                    235 TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
                                                                                                                                                          184 LSGAHTIGIAHCSSLSNRLFNFTGKGDQDPSLDSEYAANLKAFKC-TDLNKLNTTKIEMD 242
                                                                                                                                                                                              183 LSGAHTIGQARCTTFRGRIY-----GDTD--INASFAA-LRQQTCPRSGGDGNLAPIDVQ 234
                                                                                                                                                                                                                                                                            123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
303 GRINVKTGTEGEIRKHCAFLNS 324
                                                                                                                                                                                                                                       124 ARDTIVATGGPFWKVPTGRRDGVISNLTEARDNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHD
                                                                                                                                                                                                                                                                                                                                                                                                    8 LSLCLLA----LIASTHAQLQLGFYAKSCPNAEQIVLKFVHDHIHNAPSLAAALIRMHFHD 64
                                                                             PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIELLEGSVENFFAEFATSMEKM 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68124-1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 amino acids
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42.5%; Pred. No. 9.7e-57;
ative 54; Mismatches 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-868-577-13
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US-08-868-577-13
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 137;
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Best Local Similarity
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APPLICANT: Vierli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
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LENGTH: 324 amino acid
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                                                                                                                                                         183 LSGAHTIGQARCTTERGRIY-----GDTD--INASFAA-LRQQTCPRSGGDGNLAPIDVQ 234
                                                                                                                                                                                                            124
303 GRINVKTGTEGEIRKHCAFLNS 324
                                                                   243
                                                                                                                                         184
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                                                                                                                                                                                                                                                                                                                  66 CFYQGCDGSILLDA---GGEKTAGPNLNSYRGFEYIDTIKRNYEAACPGYVSCADILALA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                   6 LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHD 65
                                                                   PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIELLEGSVENFFAEFATSMEKM 302
                                                                                                                                                                                                                               ARDGTNILGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLEGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                GNVGVLTGTAGQIRRNCRVVNS 313
                                                                                                   TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
                                                                                                                                                                                                          ARDTIVATGGPFWKVPTGRRDGVISNLTEARDNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
                                                                                                                                                                                                                                                                                                                                                   LSLCLLA---LIASTHAQLQLGFYAKSCPNAEQIVLKFVHDHIHNAPSLAAALIRMHFHD 64
                                                                                                                                       LSGAHTIGIAHCSSLSNRLFNFTGKGDQDPSLDSEYAANLKAFKC-TDLNKLNTTKIEMD
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555 13th Street NW, Suite 701 East
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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N: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                      37.78;
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Pred. No. 9.7e-57;
4; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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RESULT 12 US-08-671-320-11 ; Sequence 11, Application US/08671320 ; Patent No. 5840558

GENERAL INFORMATION:

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                                                                                                          RESULT 13
US-08-868-577-11
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Best Local :
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                                                                       Patent No. 5866695
                                                                                         Sequence 11,
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INFORMATION FOR SEQ ID NO:
GENERAL INFORMATION:
APPLICANT: Vieriling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: 1125 SO. 103RD STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
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                                                                                                                                                                                 303
                                                                                                                                                                                                  292 GNVGVLTGTAGQIRRNCRVVNS 313
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                                                                                                                                                                                                                                                                                                                                                                                                124 ARDTIVATGGPFWKVPTGRRDGVVSNLTEARNNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CFVRGCDASYLLNSTINQAEKNAPPNL-TVRGFDFIDRIKSLVEAECPGVVSCADILTLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 CFVQGCDGSILLDA---GGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122
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                                                                                                                                                                                                                                                                                       TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
                                                                                                                                                                                                                                                                                                                                                                                                                    ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                     PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIQLLEGSVENFFAEFATSIEKM
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                                                                                                                                                                                GRINVKTGTEGEIRKHCAFINS
                                                                                                                                                                                                                                                                                                                          LSGAHTIGIAHCSSLSNRLFNFTGKGDQDPSLDSEYAANLKAFKC-TDLNKLNTTKIEMD
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Similarity 42.2%;
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                                                                                                                                                                                   324
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Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 604.5;
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     PEROXIDASE
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       ACTIVITY
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                                                                                                         US-08-190-029A-10
                                                                      Sequence 10, Application US/08190029A Patent No. 5736363
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 402-333-1510 INFORMATION FOR SEQ ID NO:
                                     GENERAL INFORMATION:
APPLICANT: EDWARDS, Richard Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
APPLICANT: EDWANDS, RICHARD APPLICANT: BAWDEN, Lindsey TITLE OF INVENTION: IGF-II
                                                                                                                                                                                                                                                                                                                                                                                                  123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                        243
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         303 GRINVKTGTEGEIRKHCAFINS
                                                                                                                                                                                                        292 GNVGVLTGTAGQIRRNCRVVNS 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHD 65
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                                                                                                                                                                                                                                                                                                                                      LSGAHTIGQARCTTFRGRIY-----GDTD--INASFAA-LRQQTCPRSGGDGNLAPIDVQ 234
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                                                                                                                                                                                                                                                                                                                                                                      ARDTIVATGGPFWKVPTGRRDGVVSNLTEARNNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
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NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF,
STREET: 10 S. WACKER DRIVE, SUIT

SUITE

IGF-II ANALOGUES

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RESULT 15
US-08-462-695-10
US-08-462-695-10; Sequence 10, Application US/08462695; Patent No. 5854025; GENERAL INFORMATION: EDWARDS, Richard Mark
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INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-190-029A-10
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36.5%; Score 585.5; DB 1; Length 349;
Best Local Similarity 45.6%; Pred, No. 1.5e-54;
Matches 128; Conservative 34; Mismatches 104; Indels 15; Gaps
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01389
PILING DATE: 27-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 9202401.7
PILING DATE: 05-FEB-1992
PRIOR APPLICATION DATA;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: HAN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,029;
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9116325.3
FILING DATE: 29-JUL-1991
ATTORNEY_AGENT INFORMATION:
NAME: JOHN J. MCDONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 94,062
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
               APPLICANT: EDWARDS, Ric
APPLICANT: BAWDEN, Lind
TITLE OF INVENTION: IGF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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STATE: ILLINOIS
COUNTRY: U.S.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 FRTEKDAFGNANSARGFPVIDRMKAAVESACPRTVSCADLLTIAAQQSVTLAGGPSWRVP 121
  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVP 138
                                                                                                                                                                                                                                                                                                                                                                                 MDRLYNFSNTGLPDPTLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                             RGRIYG-----DTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSR 250
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0.S.A.
BANNER & ALLEGRETTI, LTD
                                                    Lindsey
IGF-II ANALOGUES
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NAME: JOHN J. MCDONNELL
REGISTRATION NUMBER: 26,949
REFERENCE_POCKET NUMBER: 94,0)
RELECOMUNICATION INFORMATION:
TELEPHONE: 312-715-100
TELEPAY: 312-715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-695-10
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Search completed: April 26, 2003, 12:36:14
Job time: 31 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435

PRIOR APPLICATION UMBER: 08/190,029

FILING DATE: 28-FEB-1994

PRIOR APPLICATION UMBER: PCT/GB92/01389

FILING DATE: 27-UUL-1992

PRIOR APPLICATION DATA:

APPLICATION UMBER: GB 9202401.7

FILING DATE: 05-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION UMBER: GB 916325.3

PRIOR APPLICATION DATA:

APPLICATION DATA: 105-FEB-1992

PRIOR APPLICATION DATA: 1
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OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                            242
                                                                                                                                                                                                         251 RGLFHSDQELF---NGGSQDALVRQYSASASLFNADFVAAM 288
                                                                                                                                                                                                                                                                                                           182 MDRLYNESNTGLPDPTLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQ 241
                                                                                                                                                                                                                                                                                                                                                                                        198 RGRIYG------DTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 LGRRDSLQAFLDLANANLPAPFFTLPQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 LGRRDSTTASASLANSNPPPPTASLGTLISLEGRQGLS-PRDMTALSGAHTIGQARCTTF 197
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FILING DATE: 5-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVP 138
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                                                                                                                                                            KGLIQSDQELFSSPNATDTIPLVRSFANSTQTFFNAFVEAM
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Perfect score:
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Sequence 6, Appli
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Sequence 14, Appl
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TITLE OF INVENTION: Maize Defense-Inducible Genes and
TITLE OF INVENTION: Maize Defense-Inducible Genes and
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT APPLICATION NUMBER: US/10/027,559
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 357
TYPE: PAT
ORGANISM: 2ea mays
US-10-027-559-12
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US-10-027-559-12
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GENERAL INFORMATION:
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Sequence 167, App	Sequence 10094, A	Sequence 5, Appli	Sequence 893, App		~	128	Sequence 69, Appl	Sequence 5860, Ap	Sequence 11950, A	Sequence 10, Appl	Sequence 9, Appli	Sequence 23, Appl	Sequence 2, Appli	Sequence 892, App	Sequence 6, Appli	Sequence 934, App	Sequence 10446, A	Sequence 38, Appl	Sequence 405, App	Sequence 11836, A	Sequence 6, Appli	Sequence 6011, Ap	Sequence 5110, Ap	Sequence 2, Appli	Sequence 7, Appli	

ALIGNMENTS

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Their

	285	226 GNLAPIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFV 285	/RQYSASA	GSQDALV	ELFNG	GLFHSDO	NLLSRR	TDTAYET	QTPVRI	NLAPIDV	26 GI	N	VΩ	-		۲۰۱
	245	186 LSGAHTIGVSHCSSFAGINNTGDRLYNESGSSDGIDPALSKAYAFILKSICPSNSGREFP 245	LLKSICP	LSKAYAF	GIDPA	NESGSSI	TGDRLY	SFAGIN	VSHCS	SGAHTIG	86 L	ب	DЪ			۰. ۳
	225	183 LSGAHTIGQARCTTFRGRIYGDTDINASFAALRQOTCPRSGGD 225	-DTDINASFAALRQQTCPRSG	INASFA	DTD	G	RIYG-	[FRG	QARCTI	LSGAHTIGQARCTTFRG	83 Ls	<u>بر</u>	Qy			3
	185	126 ARDSVVLTGGLGYKVPSGRRDGRISNATQALNELPPPFFNATQLVDNFASKNLSLEDMVV 185	ARDSVVLTGGLGYKVPSGRRDGRISNATQALNELPPPFFNATQLVDNFASKNLSLEDMY	FNATQLV	LPPPFI	ATQALNI	DGRISN	(VPSGRI	GGLGY	RDSVVLT	26 AI	-4	рь	_		۲.
	182	123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDWTA 182	SLFGRQG	ASLGTLI	Tadadi	ASLANSI	DSTTAS	SVPLGRE	GGPTW:	RDGTNLL	23 AI	ب	Qy			1
	125	66 FVRGCDGSVLIDSTANNKAEKDSIPNSPSLRFFDVVDRAKASLEARCPGVVSCAJILAFA 125	ARCPGVVS	AKASLE	DVVDR	SPSLRFI	KDSIPN	CANNKAL	VLIDS	VRGCDGS	96 F		Db			
	122	67 FVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122	ACPGVVS	IKRNVE!	EVIDT	LNSVRGI	KTAGPN	GGI	ILLDA	FVQGCDGSILLDA	67 F		Qy	_		- j
	65	6 CLYVATLLAALLSVSASLEFGFYNKTCPSAETIVQQTVAAAFTNNSGVAPALLRMHFHDC 65	NSGVAPAL	AAAFTNI	VOOTV	CPSAET	GFYNKT	/SASLEI	AALLS	LVVATLL	6 0		Дb			j
	99	9 CLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDC 66	EQRMGASL	TQAVASE	VRAAM	CPNLQS	TFYASS	AHAQLSE	SCV1	LVAVSLL	9 - 0		Qy			
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US-10-027-559-6
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                                                                                            GENERAL INFORMATION:

APPLICANT: Takabe, Tetsuko
APPLICANT: Takabe, Tetsuko
TITLE OF INVENTION: Peroxisomal Ascorbate Peroxidase Gene Induced by High
TITLE OF INVENTION: Temperature Stress and a Trangeneic Plant Exhibiting
TITLE OF INVENTION: Thermotolerance
FILE REFERENCE: 026350-053
CURRENT APPLICATION NUMBER: US/09/870,501
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: JP 2000-172850
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
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Patent No. US20020144307A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Defense-Inducible Genes and Their
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT APPLICATION NUMBER: US/10/027,559
CURRENT APPLICATION NUMBER: 05/243,120
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
UNIVERS OF THE PRIOR PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                        SOFTWARE: PatentIn
SEQ ID NO 1
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                                                                               NUMBER OF SEQ ID NOS:
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                       ENGTH: 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 RALIAEKSCAPLMLRLAWH-------SAGTFDVSSRTGGPFGTMKHQSELAHGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLS--RRGLFH--SDQ 258
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US-09-870-501-1
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                                                                                                                                                                                                                                                                                    ; ORGANISM: Physcomitrella patens US-09-734-017A-54
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Best Local Similarity
Watches 72; Conserv
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SEQ ID NO 54
LENGTH: 176
                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                       Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: synthesis of amino acids, TITLE OF INVENTION: nucleosides FILE REFERENCE: BASF-NAE-1331-99-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lerchl, APPLICANT: Renz,
                                                                                                                                                                                                                                                                                                                      LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/171,100 PRIOR FILING DATE: 1999-12-16
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29.0%;
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; Pred. No. 3.3e-09;
42; Mismatches 112;
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                                                                                                                                                                                                   Score 136; DB 10;
Pred. No. 1.4e-05;
5; Mismatches 71;
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APPLICANT: Freund, Annette
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involv
TITLE OF INVENTION: the
TITLE OF INVENTION: synthesis of amino acids, vitamins, cofactors, nucleotides
FITE DETERMINENTION: nucleosides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 SASLANSNPPPPTASLGT--LISLFGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDT 205
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133 PTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLEGRQ-GLSPRDMTALSGAHTIGQ 191
                                                                     53 TGGP-LGTIRFGQELAHGANAGLDIAVNLLQPIKEQFP-ELSYADFYTLAGVVAVEVTGG 110
                                                                                                                                      84 TAGPNLNSVR------GFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGG 132
                                                                                                                                                                                                                                                                      30 ASSCPNLQSIVRAAMTQA-----VASEQRMGASLLRLFFHDCFVQGCDGSILLDAGGEK 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 NLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTA 147
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                                                                                                                                                                                                        2 AKSYPNVSEKYAALIEKARRKIRGMVAEKNCAPIILRLAWH------GSGTYDQ-ESK 52
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RESULT 6
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US-09-885-329-6
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TITLE OF INVENTION: Polypeptides Havin:
TITLE OF INVENTION: And Nucleic Acids
FILE REFERENCE: 10048.200-US
CURRENT APPLICATION NUMBER: US/09/885,
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/596,824
PRIOR FILING DATE: 2000-06-19
                                                                                                                                                                     Sequence 2, Application US/10095975 Publication No. US20030013182A1 GENERAL INFORMATION:
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Best Local :
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Patent No. US20020115170A1
                                                                 APPLICANT: Yaver, Debbie S.
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Isolating Genes
TITLE OF INVENTION: Microorganisms
FILE REFERENCE: 10160.200-US
CURRENT APPLICATION NUMBER: US/10/095,975
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 06/275,283
PRIOR FILING DATE: 2001-03-12
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SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                     218 TCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSRRGLFH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 APFDTVDAIIARFADVDFSVDEIVALLASHSVAAAS------HIDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 PPTASLGTLISLEGRQGLSPRDMTALSGAHTIGQARCTTERGRIYGDTDINASFAALRQQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QKPYITKYNMTPG-----DVVQFAGAVGLSNCPGAPQLEFLLGR----TAATAASPTGLIP
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Local Similarity 24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 SLRLTFHDAIGYSPALAAAGSFAGGGADGSILTFSDVEAAFFANAGLD-----EMIEL
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                                                                                                                                                                                                                                                                                                     DHELARDSRTACEWQSYVNNQSKIQSAFRAAMARMAVIG
                                                                                                                                                                                                                                                                                                                                                                               TVPES-----PLD-STPGVFDTQFFVE-TSLNGTMYPGTSGNIGEALSAIAGELRLLS
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Acids Encoding Same
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US-09-748-264A-2
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; ORGANISM: Ceriporiopsis subvermispora
US-10-095-975-2
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-748-264A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver.
SEQ ID NO 2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 376
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.1%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A BASIDIOMYCETE PEROXIDASE GENE-TRANSFERRED PLANT TITLE OF INVENTION: DECOMPOSING AND REMOVING NOXIOUS CHEMICALS USING FILE REFERENCE: 04883,0050
CURRENT APPLICATION NUMBER: US/09/748,264A
CURRENT FILING DATE: 2000-12-27
PERIOR APPLICATION NUMBER: US/09/748,264A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2000-223653 PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SECRETARY OF AGENCY OF INDUSTRIAL SCIENCE AND TECHNOLOGY APPLICANT: YOSUKE IIMURA
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Coriolus versicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 365
                                            111 NLGVDEIIDEQRPFIARHNLTTADFIQFAGAIGVSNCPGAPQLDVFIGRPDATQPAPDL-
                                                                                    101 ---IKRNVEAACPGV----VSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTASASLA 152
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                                                                                                                                                                                                                           1 MAFKTL-----ASLLSVLVTIQVASGALTRRVACPDGVNTATNAACCQLFAVRDDIQQN 54
                                                                                                                                                                                                                                                                        1 MASPTLMQCLVAVSLLSCVAHAQLSPTFYAS--SCPN-LQSIVRAAMTQAVASEQRMGAS 57
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NSNPPPPTASLGTLISLEG-RQGLSPRDMTALSGAHTIGQARCTTERGRIYGDTDINASE
                                                                                                                                                                                 L------LRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDT---- 100
                                                                                                                                    LFDGGECGEEVHESLRLTFHDAI--GISPSIA--SRGQFGGGGADGSIALFEDIETNFHA 110
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                                                                                                                                                                                                                                                                                                                  7.8%; Score 125.5; DB:10; 25.1%; Pred. No. 0.00041; ive 34; Mismatches 112;
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pred. No. 0.00034;
31; Mismatches 108;
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APPLICANT: Yaver, D
APPLICANT: McArdle
                                                                                                                                GENERAL INFORMATION:
APPLICANT: Yaver, D
APPLICANT: MCArdle
                                                                                                                                                                                Sequence 4, Application US/09885329 Patent No. US20020115170A1
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                                                                       APPLICANT: McArdle, Barbara
TITLE OF INVENTION: Polypeptides Having Peroxidase
TITLE OF INVENTION: And Nucleic Acids Encoding Sam
FILE REFERENCE: 10048.200-US
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CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/596,824
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               CURRENT APPLICATION NUMBER: US/09/88 CURRENT FILING DATE: 2001-06-19 PRIOR APPLICATION NUMBER: 09/596,824 PRIOR FILING DATE: 2000-06-19
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SOFTWARE: FastSEQ for
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NUMBER OF
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                                                                                                                                                                                                                                                                                  -TGGDNGA-
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SEQ
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ID NOS:
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23.7%;
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Query Match
Best Local Similarity
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LENGTH: 372
TYPE: PRT
ORGANISM: Phanerochaete chrysosporium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 4
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                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020138878A1
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 60/242,408
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CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TRANSGENIC PLANTS TITLE OF INVENTION: AND CELLULOSE TO FILE REFERENCE: MSU 4.1-539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sticklen, Masomeh APPLICANT: Maqbool, Shahina
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                                                                                                                                                                                                                  Local Similarity
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GFEVIDTIKRNVEAACPGV----VSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTAS
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                                                        AEAHE-----ALRMVFHDSIAISPKLQSQGKFGGGGADGSIITFSSIETTYHPNI----
                                                                                                                                                              QCLVAVSLLSCVAHAQLSPTF-YASSCPN----
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                                                                                                                            QLLAALSVALTLQVTQAAPNLDKRVACPDGVHTASNAACCAWFPVLDDIQQNLFHGGQCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09981900B
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                                                                                                                                                                                                                    Score 104.5; DB 10; Pred. No. 0.046;
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Pred. No. 0.0084;
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                                                                                            QGCDGSILLDAGGEKTAGPNLNSVR
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                                                                                                                                                                 ----LQSIVRAAMTQ 46
                                                                                                                                                                                                                                     Length 372;
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RESULT 12
US-10-101-464A-802
Sequence 802, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION UNMERR: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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; Sequence 14, Application US/09981900B
; Patent No. USS/020138878A1
; GENERAL INFORMATION:
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Best Local S
Matches 57
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PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 371
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APPLICANT: Madbool, Shabina B
APPLICANT: Madbool, Shabina B
APPLICANT: Dale, Bruce E
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH DEGRAD TITLE OF INVENTION: AND CELLULOSE TO FERMENTABLE SUGARS
FILE REFERENCE: MSU 4.1-539
CURRENT APPLICATION NUMBER: US/09/981,900B
CURRENT FILING DATE: 2002-03-18
  PRIOR APPLICATION NUMBER: 09/704,302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 LGTLIS-LFGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 QKHGVTPG-----DFIAFAGAVALSNCPGAPQMNFFTGRAPATQPA----PDGLVPEPFHS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 IRLVFHDAIAISPAMEPQASSVRGADGSIMIFDEIETNFHPNI----GLDEIVRLQKPFV 124
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Similarity 22.6%; Pred. No. 1.
57; Conservative 32; Mismatche
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APPLICANT: Murphy, Dennis J.

APPLICANT: Murphy, Dennis J.

APPLICANT: Maffa III, Anthony M.

APPLICANT: Bylina, Edward J.

APPLICANT: Bylina, Edward J.

APPLICANT: Coleman, William J.

APPLICANT: Coleman, William J.

APPLICANT: Using Same

FITLE OF INVENTION: Using Same

FILE REFERENCE: HER-0040

CURRENT APPLICATION NUMBER: US/09/782,906

CURRENT APPLICATION NUMBER: 50/195,001

PRIOR APPLICATION NUMBER: 50/25

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 639
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PRIOR APPLICATION NUMBER: 09/228,986
PRIOR ELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 802
LENGTH: 345
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US-09-782-906-5
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US-10-101-464A-802
                                                                                                                                                   ; OTHER INFORMATION: No. US20010051369Alel Sequence US-09-782-906-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09782906 Patent No. US20010051369A1 GENERAL INFORMATION:
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                                                 Query Match
Query Match
Best Local Similarity 20.5%; Pred. No. 8.6;
Matches 63; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 34
TYPE: PRT
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LSGAHTIGQARCTTERGRIYGDTDINASEAALRQQTCPRSGGDGN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 CGSSPLAACSLSGTSPPASSSLTVPSNPSSMPETPAIGP-----GQKHRQKGLSTGAIVA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 --DSTTASASLANSNPP-------PPTASLGTLISLFG----RQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 RL-LTLRLQSNLLSGEVPDLSVSLKNLKELNLTNNELYGHLPDGLLRKFGVRSFVGNEGL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LNGTVTPLANCTNLKLLYLAGNDFSGEIPPEISSLRRLLRLDISDNNIRGVIPGEVRGLS 173
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  64 HDCFVQGC----DGSILLDAG--GEKTA-----
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     ----GPNLNSVRGFEVIDTI----- 101
                                                                                                  DB 10;
                                                    Indels 125;
                                                                                                  Length 639;
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CURRENT APPLICATION NUMBER: US/10/101.464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION UNBER: 09/704.302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION UNBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 1900-01-11
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 890
SEQ ID NO 890
LENGTH: 804
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Sequence 890, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102002
409 LSDLQRLDLSNNNLTGSLPLSISHIEDLQELDLYNNNIFGTIPNTISLTSLQILDLSKNN 466
                                            170 ---FGRQGLSPRDMTA---LSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSG 223
                                                                                              350 RS-SISIPPSITDTDLVYLDLSNNQLIGSLPRNIGQLSSLQSLVLSNNNLIGSLPHNIGQ 408
                                                                                                                                                131 GGPTWSVPLGRRDSTTASASLANS----NPPPPTASLGTLISL-------
                                                                                                                                                                                                  293 ALKGSGNKLSGP-IPSVMGLMKSISTIDLSNNSLTGRIPTTLVNCTQLYELYL--STNNL 349
                                                                                                                                                                                                                                                                                                       234 PTSLA-NCTSLTDLVISSNNLSGPIPSEFSGLVSLKFLFLDDNSISGSIPTSLVNCTSLF 292
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                                                                                                                                                                                                                                                                                                                                                      26 PTFYASSCPNLQSIVRAA--MTQAVASEQRMGASLLRLFFHDCFVQG-----CDGSI 75
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                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 84.5; DB 9; Length 804; ; Pred. No. 12; 37; Mismatches 122; Indels 47;
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 4999
TYPE: PRT
ORGANISM: Actinoplanes sp.
US-09-976-059-14
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Search completed: April 26, 2003, 12:43:24 Job time: 46 secs
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Patent NO. US20020164747A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
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Best Local :
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APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-ECT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                           1740 RVAQFASPGFDMFVDEWSMAL-----LAGAALTFVPPERRLGADLAAFLAEYGVTHATLP 1794
                                                                                        1901 LNRAGLTAERFVACPFEPGERMYRTGDV 1928
                                                                                                                                                                      1849 WRAE----AGDWGSVAPIG--TPVPNLRAYVLDGWLRPVPVGADGELYVSGA--GLARGY 1900
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58; Conservative
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27.98;
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Pred. No. 1.9e+02;
21; Mismatches 94; Indels
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-MODEL-frame+_D2n.model -DEV=x1h
-MODEL-frame+_D2n.model -DEV=x1h
-Q-/Cgn2_1/USPT0_spool/US10047825/runat_26042003_112042_7644/app_query.fasta_1.455
-DB-CenEmbl -QFMT-fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MATRIX=01190 -TRANS-human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE-quality -THR_MIN=16 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US10047825_@CGN_11_1687_@runat_2604003_112042_7644 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
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and is score Pred. No. greater derived is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-JUL-1994) Annette H. Ross,
Botany, St. Lucia, Brisbane, Queensland,
Location/Qualifiers
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KNVEAACPGVVSCATIVPLAARPGPNLLGGPTWNVPLGRRDSTTAMLSLANQNLPPPT
SLGTLISLFGGRLSARDMIALSGAHHAQARCTTFRGRIYGDTNIDASFAALQQQTCPR
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440 c 374 g
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/protein_id="AAA20472.1"
/db_xref="GI:520568"
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/note="expressed in location of the control 
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/clone_lib="lambda gt-10"
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/cultivar="Biloela"
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
                                                                                                                                                                                                           CGC 77674
                                                                                                                                                                                                                                             Arg 124
 Phaseolus vulgaris.
Phaseolus vulgaris
Eukaryota; Viridiplantae;
                                                                          AF149279 835 h
Phaseolus vulgaris peroxidase
AF149279
AF149279.2 GI:6573300
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2 (bases 1 to 160562)
Sasaki.T., Matsumoto,T. and Katayose,Y.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Location/Qualifiers
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33079 c 35854 g 45
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/chromosome="2"
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/cultivar="Nipponbare"
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2 clone
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Tracheophyta;
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                                                                                                                                                                            p15a gene; peroxidase.
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Justesen, A.F., Jespersen, H.M. and Welinder, K.G. Analysis of two incompletely spliced Arabidopsis cDNAs encodinovel types of peroxidase plochim, Biophys. Acta 1443 (1-2), 149-154 (1998)
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TERTAGFNLNLQGfEVIDNAKTQLEAACPGVVSCADILALAARDTVILTQGTGWQVPT
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Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT
CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl,
Jeffrey L. (US); Eulgem, Thomas (US)
Location/Qualifiers
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
                                                                                                                                               Sequence
AX412383
Glazebrook,J.,
                                                                                                thale cress.
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Submitted (11-MAR-1997) A.F.
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Justesen, A.F.
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Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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MAPRGNFNVQFARSMVKMSNIGVKTGTNGEIRRVCSAVN"
199 c 218 g 273 t
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/dev_stage="etiolated seed
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis,
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Syngenta Participations AG (CH); UNIVERS:
CHAPEL HILL (US); Glazebrook, Jan (US);
Jeffrey L. (US); Eulgem, Thomas (US)
Location/Qualifiers
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Sequence 342 from Patent
AX412578
AX412578.1 GI:21445036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T. Plant genes, the expression of which are altered by path
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA Malibu, CA 90265, USA This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have
                                                                                                                                                                                                                                                                           Genome Biol. (2002) In 2 (bases 1 to 1271)
                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1271)
Haas, B. Tolfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana clone 23349
                                                                                                                                                       Direct Submission
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Brover, V., Troukhan, M.,
                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                 Full-Length cDNA from Arabidopsis thaliana
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Flavell, R. and

Flavell, R.

and

linear

PLN 26-JUN-2002

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Patent: WO 0222675-A 577 21-MAR-2002;
Syngenta Participations AG (CU); UNIVERSI
CHAPEL HILL (US); Glazebrook, Jan (US);
Jeffrey L. (US); Eulgem, Thomas (US)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1287 bp mRNA Arabidopsis thaliana AT5g64120/MHJ24_10 AF428274 aF428274.1 GI:16226218 FII_CDNA.
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Ishida, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Warusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                         Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thallana.
Arabidopsis thallana
Arabidopsis thallana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Arabidopsis.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Cheuk,R., Chen,H., Kim,C.J., Koesema,E.,
                                                                                                                                                                                                                                                                            Unpublished
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LQGFEVIDNAKTOLEAACPGVVSCADILALAARDTVILTQGTGQVPTGRRDGRVSLA
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WTDPATRPIVQQLMAPRSTFNVEFARSMVRMSNIGVVTGANGEIRRVCSAVN"
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RESULT 13
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Query Match:
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                                        cationic peroxidase.
A.hypogaea, cDNA to mRNA.
Arachis hypogaea
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; eurosids I; Fabales; Fabaceae; Papili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFI CONAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
Aeschynomeneae; Arachis.
1 (bases 1 to 1330)
                                                                                                                                                                                          M37637.1
                                                                                                                                                                                                                    A.hypogaea cationic M37637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                                       ARCPNC2
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WTDPATRPIVQQLMAPRSTFNVEFARSMVRMSNIGVVTGANGEIRRVCSAVN"
1 302 c 282 g 345 t
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Matches:
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BASE COUNT
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluAlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp 125
                                                                                                                                                                                                                                                                                                                              1389 bp mRNA linear PLN 24-MAR-2002
Gossypium hirsutum bacterial-induced gaiacol peroxidase (pod29)
mRNA, complete cds.
AF485258
AF485268.1 GI:19698451
                                                                                                                                                                                           Gossypium hirsutum.
Gossypium hirsutum.
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvacles; Malvaceae; Gossypium.
Lobases I to 1389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Draft entry and computer-readable sequence kindly submitted by R.Esnault, 08-AUG-1990.
Institut des Sciences Vegetales
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Molecular cloning of complementary DNAs encoding two cationic peroxidases from cultivated peanut cells
Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8874-8878 (1990)
                                                                                          Submitted (20-FEB-2002) UR Resistance, Montpellier 34032, France
                                                                                                                                 Delannoy.E., Assighetse,K., Jalloul,A., Marmey,P., Daniel,J.-F., Geiger,J.-P. and Nicole,M.
Direct Submission
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/cultivar="Reba B50"
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(bases 1 to 1400)

Justesen, A.F., Jespersen, H.M. and Welinder, K.G.

Analysis of two incompletely spliced Arabidopsis cDNAs encodin novel types of percyidase
Biochim, Eiophys. Acta 1443 (1-2), 149-154 (1998)

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1 (bases 1 to 1400)

Welinder, K.G., Jespersen, H.M., Kjaersgaard, I.V.H., Justesen, A.F., Oestergaard, I., Abelskov, A.K., Jensen, R.B., Hansen, L.N. and Rasmussen, S.K.
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Arabidopsis thaliana
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Justesen, A.F.
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Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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RESULT 2 AAC48650 ID AAC48650; XX AC AAC48650; XX AC AAC48650; XX AC AAC48650; XX A Fabidopsis thaliana DNA fragment SEQ XX Hybridisation assay; genetic mapping; XX Hybridisation assay; genetic mapping; XX Protein identification; signal transd, XX Arabidopsis thaliana. AR AR AR AR AR AR AR BP BP C5-FEB-2000; 2000EP-0301439. XX AR AR AR AR BP C5-FEB-1999; 99US-0121825. PR C5-FEB-1999; 99US-0121825. PR C5-MAR C999; 99US-0125746. PR C5-MAR C999; 99US-0125746. PR C6-AR C999; 99US-012844. PR C6-AR C999; 99US-013044. PR C6-AR C6-MAY C999; 99US-013344. PR C6-MAY C999; 99US-013348. PR C6-MAY C999; 99US-013248. CR C6-MAY C999; 99US-013248. C7 C7 C7 C7 C7 C7 C7 C7 C7 C	US-10-047-825-4 (1-313) x AAC46841 (1-1041) QY 106 GluAlaAlaCysProglyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp	PR 21-OCT-1999; 99US-0160815. PR 22-OCT-1999; 99US-0160980. PR 22-OCT-1999; 99US-0160981. PR 25-OCT-1999; 99US-0161404. PR 25-OCT-1999; 99US-0161405. PR 25-OCT-1999; 99US-0161359. PR 26-OCT-1999; 99US-0161359. PR 26-OCT-1999; 99US-0161350. PR 26-OCT-1999; 99US-0161920. PR 28-OCT-1999; 99US-0161920. PR 28-OCT-1999; 99US-0161921. PR 28-OCT-1999; 99US-0162142. Alignment Scores: Pred. No.: Score: Pred. No.: Score: Pred. No.: Score: 100.008 Best Local Similarity: 100.008 Milliarity: 100
mapping; gene expression control; il transduction pathway; termination sequence; ss.	1) laAspIleLeuAlaLeuAlaAlaArgAsp 125	Length: 1041 Matches: 20 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0
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    (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase coniferol glucosyl transferase (CCT), coniferin beta-glucosidase laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffele acid methyl transferase, caffeoyl COA methyl transferase, coumerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, fl glucosyl transferase, flavenoid hydroxylase, and isoflavone reduc
                                                                                                                                         encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
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14-JUL-1999;
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Pinus radiata;
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99US-0143811.
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which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin biosynthetic pathway, and for producing a plant having altered lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
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Sequence 364 BP; 98 A; 111 C; 69 ç; 86 T; 0 other;

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Alignment Scores: Pred. No.:
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US-10-047-825-4 (1-313) x AAA68190 (1-364)

RESULT 5 AAA68156

AAA68156 standard; DNA; 512 ВP

AAA68156

24-OCT-2000 (first entry)

Eucalyptus grandis peroxidase nucleotide sequence SEQ ij NO:249

Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis; Pinus radiata; Monterey pine; ds.

Eucalyptus grandis

20-APR-2000

06-OCT-1999; 99WO-NZ00168

09-OCT-1998; 14-JUL-1999; 98US-0169789. 99US-0143811.

(GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD

Bloksberg LN, Havukkala IJ;

WPI; 2000-317962/27

Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and

Claim 1; Page 133; 213pp; English

The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase (4CL), coniferol glucosyl transferase (CGT), coniferol glucosyl transferase (CGT), coniferon glucosyl transf

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The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxidase nucleotide sequence SEQ ID NO:362
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lignin biosynthetic pathway; Eucalyptus grandis Monterey pine; ds.
                                                                                                                                                                                                               Havukkala
                                                                                                                                                                                                                                                                                       98US-0169789.
99US-0143811.
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                                                                                                                     in lignin-biosynthetic especially eucalyptus, composition and
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pathway useful reand pine species

polynucleotide encoding enzymes involved in lignin-biosynthetic ay useful for producing transgenic plants especially eucalyptus ine species having altered lignin content, composition and

Novel

Claim 1; Page

183;

213pp; English.

describes isolated

polynucleotides

proteins

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Pred. No.:
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14-JUL-1999;
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                                                                                                                                                           Bloksberg LN,
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                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                             Pinus
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99US-0143811.
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R CHALLENGE FORESTS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                             pathway;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peroxidase; active oxygen resistance; transgenic plant; environmental stress.
                                                                                                                                                                                                                                                                                                                                                                     (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 717 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCCTGGGGTCGTCTTGCGCCCGACATCTTGGCCTTGGCCGCTCGGGAT
                                                                                                                                  4; Page
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밁 ð Query DB:

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US-10-047-825-4 (1-313) x AAH45565
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Query Match:
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                                                                                     Alignment Scores:
                                                                                                                             peroxidase. The gene is useful for the development of a plant highly resistant against active oxygen which is formed under various environmental stress conditions. This sequence represents a peroxidar related DNA fragment.
                                                                                                          Sequence 1090 BP;
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밁 AAC45025 standard; DNA; 1106 ВP 458

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AAC45025;

18-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ IJ NO: 45019

metabolic pathway; promoter; termination sequence; Hybridisation assay; ger protein identification; genetic mapping; gene expression
on; signal transduction pathway; 88 control;

Arabidopsis thaliana.

06-SEP-2000

25-MAR-1999; 29-MAR-1999; 01-APR-1999; 06-APR-1999; 08-APR-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-FEB-1999; 05-MAR-1999; 25-FEB-2000; 2000EP-0301439

21-APR-1999; 23-APR-1999; 23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999; 19-APR-990S-0129845 990S-0130047 990S-0130649 990S-0130510 990S-0131449 990S-0132048 990S-0132484 990S-0132484 990S-0132485 990S-0132485 99US-0128234 99US-0128714

11-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 99US-0132863. 99US-0134256. 99US-0134218. 99US-0134219. 99US-0134221. 99US-0134370. 99US-0134768.

This invention relates to a peroxidase derived from a Paraquat resistant callus. Included in the invention are the gene encoding the peroxidase, a vector containing the gene, and a method for the preparation of the

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RESULT 1:
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28-OCT-1999;
29-OCT-1999;
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                      cDNA clones (AAT66684-87) respectively code for soybean peroxidases SEPal, SEPal, SEPbl and SEPb2 (AAM16607-10). Plant peroxidase specific primer PSF (AAM166079) was generated from the conserved distal haem ligand (AAW16603) in all plant peroxidases, and was used to generate a peroxidase gene probe. Primary hybridisation screening using the probe yielded 25 clones. Il positive clones were recovered after 2 rounds of PCR using PSP and a T7 vector.
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P-PSDB; AAW16610.
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                                                                                                                                                                                                                   Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                        Vierling RA
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                                                                                                                                                                                                                                                          lated soybean peroxidase genes - useful for developing quantification and monitoring of peroxidase activity
    and
                                                                                                                                                                                                                Page 43-44; 63pp; English.
    4 clones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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102..977
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Matches:
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    and SEPb2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV81423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysed. The soybean peroxidase genes can be used to develop products for the quantification and monitoring of peroxidase activity, e.g. in assays such as ELISA, PCR, plant breeding programmes, pulp and paper bleaching, on-site waste destruction, soil remediation and organic synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1167 BP; 385 A; 232
This cDNA clone codes for novel soybean peroxidase SEPb2 (see AAW67734). 4 Clones, designated SEPa1, SEPa2, SEPb1 and SEPb2 (see AAV81420-23) were isolated from a soybean cv. Resnick seedling cDNA library using a plant peroxidase specific primer (see AAV81424) and 3'RACE. Genomic clones (see AAV81418-19) for SEPa1 and SEPb1 were also obtained. The coding regions of SEPa1 and SEPa2 exhibit 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV81423;
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                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulp; paper;
                                                                                                    New soybean peroxidase genes - useful, e.g. in pulp and paper bleaching, on site waste destruction and soil remediation
                                                                                                                                                                         Vierling
                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peroxidase;
                                                                              Example 8; Page 48-49; 78pp; English.
                                                                                                                                        WPI; 1999-070273/06
P-PSDB; AAW67734.
                                                                                                                                                                                                (INDI-) INDIANA
                                                                                                                                                                                                                       04-JUN-1997;
                                                                                                                                                                                                                                             04-JUN-1998;
                                                                                                                                                                                                                                                                    10-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 TGCCCAGGTGTGGTCTCTTGTGCTGACATCCTTGCTCTAGCAGCAGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEPb2; soybean; transgenic plant; immunoassay; ass; bleaching; bioremediation; soil decontamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                   3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    share 47% amino acid identity. The peroxidases are useful in pul and paper bleaching, on site waste destruction, soil remediation, organic synthesis and diagnostic chemistries. Soybean peroxidase has advantages over chlorine bleach, being cheaper, more environmentally friendly, and producing hydroxyl ions with twice the oxidising power of chlorine ions. The plant enzyme is cheap and easy to produce. The invention also relates to immunoassays
                                                                             Vierling
                                                                                                                                                                                                 US5840558-A
                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                   Sg
                                                                                                                                                                                                                                                                                                                                         5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid identity, the coding regions of SEPbl and SEPb2 share 95% amino acid identity, and the coding regions of SEPal and SEPb1 share 47% amino acid identity. The peroxidases are useful in pulp and paper bleaching, on-site waste destruction, soil remediation,
        cDNA encoding soya peroxidase SEPal - useful for producing recombinant peroxidase
                                           WPI; 1999-034041/03.
P-PSDB; AAW81496.
                                                                                                                            27-OCT-1995;
                                                                                                                                                                         24-NOV-1998
                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                             Soybean peroxidase;
                                                                                                                                                  27-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean peroxidase SEPb2 polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV69276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV69276 standard; cDNA; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1167 BP; 385 A; 232 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide assays which utilise soybean peroxidase as marker.
                                                                                                    (INDI-)
                                                                                                                                                                                                                                                                                                                                                                                                  industry; diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369
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                                                                                                                                                                                                                                                                                          "SEPb2
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                                                                                                                                                                                                                                                                                        polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative: Mismatches: Indels:
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                   This invention relates to a peroxidase derived from a Paraquat callus. Included in the invention are the gene encoding the per a vector containing the gene, and a method for the preparation peroxidase. The gene is useful for the development of a plant h resistant against active oxygen which is formed under various environmental stress conditions. The present sequence represent
                                                                                                          Claim 3; Page 13-15; 23pp;
                                                                                                                                               Peroxidase derived from Paraquat-resistant callus, it, used for the development of plants resistant to
                                                                                                                                                                                                                                                   30-SEP-1999;
                                                                                                                                                                                                                                                                            30-SEP-1999;
                                                                                                                                                                                                                                                                                                                             JP2001095585-A.
                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                            environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH45561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA encodes a soybean peroxidase SEPb2 polypeptide. The invention provides four cDNA sequences (AAV69273 to AAV69276) encoding soybean peroxidases SEPa1, SEPa2, SEPb1 and SEPb2 (AAW81493 to AAW81496) respectively. An expression vector containing the SEPa1 cDNA sequence can be used to transform host cells for the recombinant production of the peroxidase. The peroxidase is useful in industries and diagnostic
                                                                                                                                                                                       P-PSDB; AAG64621.
                                                                                                                                                                                                  WPI; 2001-360494/38
                                                                                                                                                                                                                          (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                     10-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH45561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1167
                                                                                                                                     formed under environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                                          Peroxidase; active oxygen resistance; transgenic plant; environmental stress; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Columns 35-38; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Мо.:
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Matches:
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the preparation of the
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                                                                                   US-10-047-825-4 (1-313) x AAH45568
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                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                     This invention relates to a peroxidase derived from a Paraquat resistant callus. Included in the invention are the gene encoding the peroxidase, a vector containing the gene, and a method for the preparation of the peroxidase. The gene is useful for the development of a plant highly resistant against active oxygen which is formed under various environmental stress conditions. This sequence represents a PER4 peroxidase related cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peroxidase derived from Paraquat-resistant callus, and gene encoding it, used for the development of plants resistant to active oxygen formed under environmental stress -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1191
                                                                                                                                                                                                                                                       Sequence 1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase; active oxygen resistance; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PER4 peroxidase related cDNA SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH45568 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 20-21; 23pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TOYT ) TOYOTA JIDOSHA KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2001
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                    408
                    TGTCCTGGAGTTGTTTCCTGTGCTGATATTCTTGCTCTAGCTGCTCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                       B₽;
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                                                                                                                                                                                                                                                       364 A;
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Best Local Similarity:
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14-JUL-1999;
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99US-0143811.
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The present invention describes isolated polynucleotides and proteins ce encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (CCR), phenylalanine ammonia-lyase (PAL), cinnamyl alcohol dehydrogenase (PAL), cinnamyl-CoA reductase. CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC laccase, peroxidase, ferulate-5-hydroxylase (FSH), alpha-amylase, CC commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenold hydroxylase, and isoflavone reductase, CC which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC content, composition and structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any CC content, composition and structure. They can be used for designing probes cand primers useful for detecting similar DNA and RNA sequences in any CC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any CC content can be efficiently conten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; lignin; lignin biosynthetic pathway; Eucalyptus. Pinus radiata; Monterey pine; ds.
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Db 173 CGCATGGGTGCTTCTCTCCTGCGCCTCTTCTTCATGATTGCTTCGTC 220

Search completed: May 3, 2003, 13:57:21 Job time: 194 secs

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US-09-615-192A-366

Sequence 366, Application US/09615192A Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka

FILE REFERENCE: 11000.1003c4u
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11

TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U

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Result
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-615-192A-366

US-09-615-192A-349

US-09-615-192A-350

US-09-615-192A-350

US-08-671-320-16

US-08-688-577-16

US-09-615-192A-353

US-08-671-320-14

US-08-868-577-14
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Sequence 249, App
Sequence 362, App
Sequence 350, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 353, App
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Sequence
   App1
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US-09-615-192A-249

Patent No.

249, Application US/09615192A 5. 6410718

GENERAL INFORMATION:

APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant
FILE REFERENCE: 11000.1003c4U

for the Lignin Content US-10-047-825-4 (1-313) x US-09-615-192A-366 (1-364)

182 AlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArg 198

Query Match: DB:

Percent Similarity: Best Local Similarity:

1.92e-08 17.00 100.00% 100.00% 5.43%

Matches: Conservative: Mismatches: Indels:

364 17 0 0

Score:

Alignment Scores: Pred. No.:

; SOPTWARE: FastSEC ; SEQ ID NO 366 ; LENGTH: 364 ; TYPE: DNA ; ORGANISM: Pinus r US-09-615-192A-366

NUMBER OF SEQ ID NOS:

FastSEQ for Windows Version 3.0

PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09

CGNMENTS

Percent Similarity:
Best Local Similarity:
Query Match:

2.67e-08 17.00 100.00% 100.00% 5.43%

Length:
Matches:
Conservative:
Mismatches:

512 17 0 0

Alignment Scores:
Pred. No.:
Score:

; ORGANISM: Eucalyptus US-09-615-192A-249

grandis

SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 249 LENGTH: 512 TYPE: DNA

NUMBER OF SEQ ID NOS:

405

FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09

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; Sequence 362, Application US/09615192A
; Patent No. 6410718
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-350
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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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LENGTH: 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 350, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION:
                                                                 SEQ ID NO 350
LENGTH: 717
                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                    FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
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                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 CysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp 125
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Matches:
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RESULT 5
US-08-671-320-16
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Query Match:
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             Alignment Scores:
                                          US-08-671-320-16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 402-398-9005 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 68124-1076
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO.
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VIERLING JR, RICHARD A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
No.:
                                                                                  FEATURE:
                                                                                                                            FEATURE:
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: OMAHA
                                                                      NAME/KEY:
                                                                                                                                          LOCATION:
                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                           NAME/KEY:
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978..1167
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39..977
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1..38
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39..101
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Matches:
Conservative:
Mismatches:
Indels:
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Length:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Percent Similarity:
Best Local Similarity:
                                                           Alignment Scores:
                                                                                         ; NAME/KEY:
; LOCATION:
US-08-868-577-16
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                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: WORDPERCE 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8
FILING DATE: 04-UN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                    OLECULE TYPE: cDNA
                                                                                                                                                  NAME/KEY:
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555 13th Street NW, Suite 701 East
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Eucalyptus grandis US-09-615-192A-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-615-192A-353; Sequence 353, Application US/09615192A; Patent No. 6410718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08671320 Patent No. 5840558
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VIERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 337
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: 1125 SO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 CGCATGGGTGCTTCTCTCCTGCGCCTCTTCTTCATGATTGCTTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 ArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheVal
                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                             STREET:
APPLICATION NUMBER:
                                                                                                                                             COUNTRY: US
ZIP: 68124-1076
                                                                                                                                                                                                           CITY: OMAHA
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                                                                                                                                                                                                                               SUITE 330
                                                                                                                                                                                                                                                                                                             VIERLING JR, RICHARD A

VENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN

VENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
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US/08/671,320
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Matches:
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Indels:
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US-08-868-577-14
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-671-320-14
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Vierling Jr., Richard A
APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: 555 13th Street NW, Suite 701 East
STREET: 555 13th Street NW, Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                                     sequence 14, Application US/08868577 Patent No. 5866695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JOUDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
TELEPAX: 402-398-9005
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                             COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
FEATURE:
                                                                              SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
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NAME/KEY:
                ATTORNEY/AGENT INFORMATION:
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                             APPLICATION NUMBER: US/08/868,577
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                      STREET: 555 13th
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1191 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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Jondle, Robert J.
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999..1191
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1..59
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123..998
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-047-825-4 (1-313) x US-08-868-577-14 (1-1191)
                                                                                                                ;
US-08-868-577-14
                                                                               Pred. No.:
                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                               TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
                                                                                                                                     FEATURE:
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999..1191
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1..59
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60..998
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60..122
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Matches:
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Indels:
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Search completed: May Job time : 48 secs 3, 2003, 14:53:14 밁 QΥ

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Minimum DB
Maximum DB
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-Q-/cgn2_1/USPY0_spool/US10047825/runat_26042003_112044_7756/app_query.fasta_1.455
-DB-Published_Applications_Na_CgrWT-fastap_-SUFFIX=rupb_-MINMATCH=0.1
-DB-Published_Applications_Na_CgrWT-fastap_-SUFFIX=rupb_-MINMATCH=0.1
-COOPCL-0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=-01igo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=16
-ALIGN=15 -MODE-LOCAL -CUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLENN-0
-MAXLENN-200000000 -USRR-US10047825_@CGN_1_84_@runat_26042003_112044_7756
-NAXLENN-200000000 -USRR-US10047825_@CGN_1_84_@runat_26042003_112044_7756
-NCPU=6 -CCPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG
-DEV_TIMEDUT=100 -MARNL_TIMEDUT=30 -THERADS=1 -XGAPD=60 -XGAPDEXT=60 -FGAPDP=6
-DEVENT=7 -YGAPDP=60 -YGAPDEXT=60 -DELDEXT=7
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Perfect score:
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Ygapop 60.0
Fgapop 6.0
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
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/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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                                                                                                                                     Length DB
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271
334
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     US-09-938-842A-1596
US-09-938-842A-1518
US-09-878-574-12464
US-09-878-574-744
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3424.513 Million cell updates/sec
Sequence 1596, Ap
Sequence 1518, Ap
Sequence 12464, A
Sequence 744, App
                                                                                                                                  Description
                                            APPLICANT: KIEDEN, JOEÍ
APPLICANT: KIEDEN, JOEÍ
APPLICANT: KIEDEN, JOEÍ
APPLICANT: KIEDEN, JOEÍ
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1518
LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/3
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1596
LENGTH: 960
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1596
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1518, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
  ORGANISM: Arabidopsis thaliana
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5.55e-11 20.00 100.00% 100.00% 6.39%

Conservative: Mismatches: Indels: Length: Matches:

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PRIOR	PRIOR	PRIOR	; CURREN	; CURREN	FILE R	; TITLE	TITLE	; APPLICANT:	APPLICANT:	APPLICANT:	; APPLIC	; GENERAL INFORMATION:	; Patent No. US20020160378A1	; Sequence	US-09-938-842A-1596	RESULT 1		7	თ	տ	
APPLICA:	FILING	APPLICA	T FILING	T APPLIC	EFERENCI	OF INVE	DE INVE				APPLICANT: Harper, Jeff	INFORM	No. US2	e 1596,	-842A-1			16	17	17	
NOL	DATE	NOL	3 DAT	CATIC	3: SC	MIION	TION	Zhu, Tong	Wang, Xun	eps,	rper,	ATION	00201	Appl	96			5.1	ъ •	UT .	
NUMBER:	PRIOR FILING DATE: 2000-08-24	NUMBER:	CURRENT FILING DATE: 2001-08-24	N NUMBER	FILE REFERENCE: SCRIP1300-3	I: SAME,	I: STRESS	ong	Xun	Kreps, Joel	Jeff		.60378A1	ication					1074	-	
us 6	-24	US 6	-08-	:: US	ú	ANI	-REC							US/C				10	ω	φ	
PRIOR APPLICATION NUMBER: US 60/264,647		PRIOR APPLICATION NUMBER: US 60/227,866	-24	CURRENT APPLICATION NUMBER: US/09/938,842A		TITLE OF INVENTION: SAME, AND METHODS OF USE	TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING							Sequence 1596, Application US/09938842A			ALIGNMENTS	10 US-09-878-574-8092	US-09-938-842A-2656	US-09-938-842A-2693	
							LANTS,											92	56	93	
	-						TRANSGENIC											Sequence 8092, Ap	Sequence 2656, Ap	Sequence	•
							PLANTS											e 8092,	2656,	2693,	
							CONTAINING											Āρ	Āρ	Aρ	

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                         APPLICANT: Byrum, Joseph R.

APPLICANT: The Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION UMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                         US-09-878-574-744
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Best Local Similarity:
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065809H1
US-09-878-574-12464
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT EILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 12464
LENGTH: 271
                                                                         SEQ ID NO 744
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Sequence 744, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12464, Application Patent No. US20020110548A1
                                                                                           NUMBER OF SEQ ID NOS: 15775
                                TYPE: DNA
         ORGANISM: Glycine max
                                                      ENGTH:
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Best Local Similarity:
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US-09-938-842A-2656
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PRIOR DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2693
TYPE: DNA
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                         Sequence 2656, Application US/09938842A Patent No. US20020160378A1
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Yun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILE REFERENCE: SCRIP1300-3
CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US/09/938,842A
CURRENT FILLING DATE: 2001-08-24
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Sequence 8092, Application US/09878574

Patent No. US20020110548A1

GENERAL INCOMMATION

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)8

CURRENT APPLICATION UNMBER: US/09/878,574

CURRENT APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PILING DATE: 1999-06-14

INUMBER OF SEQ ID NOS: 15775

SEQ ID NO 8092

LENGTH: 285

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 70110073991
                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2656
LENGTH: 1074
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Pred. No.:
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Search completed: May 3, 2003, 15:30:52 Job time: 110 secs
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ALIGNMENTS

A; Reference number: Z16599

A; Accession: T09166

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: presences: EMBL:Y10467

A; Cross-references: EMBL:Y10467

A; Cross-r probable peroxidase (EC 1.11.1.7) (clone PC23) - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-.
C;Accession: T09166
R;Simon, P. submitted to the EMBL Data A; Reference number: Z16599 Query Match
Best Local Similarity
Matches 195; Conserv 304 IRRNCRVVN 312 11 VAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQG 70 YKNLIAKRGLLHSDQELYNGGSQDALVTRYSKSNAAFAKDFVAAIIKMGNISPLTGSSGE AHTIGQARCTTERGRIYGDTDINASFAALRQQTCPRSG--GDGNLAPIDVQTPVRFDTAY 243 GTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSG 185 FTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQ 303 GVFLLGGPSWKVPLGRRDARTASLTAATNNLPPASSSLSNLTTLFNNKGLSPKDMTALSG Conservative 62.6%; Library, 46; Score 1004.5; Pred. No. 5.7e 46; Mismatches January 11-Jun-1999 #text_change 20-Jun-2000 .7e-74; nes 61; DB 2; Indels Length 309; 7; Gaps 180 60 Ψ

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peroxidase (EC 1.11.1.7) - flax (fragment)
C:Species: Linum usitatissinum (flax)
C:Species: 1-May-1999 #sequence_revision 21-May-1999 #text_change 04-Mar-2000
C:Accession: T08121
R:Omann, F: Tyson, H.
submitted to the EMBL Data Library, February 1998
A:Description: CDNA sequence of a basic peroxidase (FLXPER4) in flax.
A;Reference number: Z16366
A;Reference number: Z16366
A;Recession: T08121
A;Status: precliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-305 < COMA>
A;Cross-references: EMBL:AF049881; NID:g2944416; PIDN:AAC05277.1; PID:g2944417
A;Experimental source: cv. Stormont Cirrus
C:Genetics:
A;Genetics:
A;Genetics: A;Genetics:
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;33-103/Disulfide bonds: #status predicted
F;50/Active site: Arg #status predicted
F;56-61/Disulfide bonds: #status predicted
F;56-61/Disulfide bonds: #status predicted
F;56-61/Disulfide bonds: #status predicted
F;56-61/Disulfide bonds: #status predicted
                                                                                                                                                                    probable peroxidase (EC 1.11.1.7) (clone PC44) - spinach C; Species: Spinacia oleracea (spinach) C; Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text C; Accession: T09164
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A; Residues: 1-323 <SIM>
A; Cross-references: EMBL:Y10465
                                        A;Status: preliminary; translated A;Molecule type: mRNA
                                                                                    A; Reference number: A; Accession: T09164
                                                                                                        submitted to the EMBL Data Library, A; Reference number: Z16599
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                                                                                                                                                                  Accession: T09164
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109-301/Disulfide bonds: #status predicted 188-213/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 TIGQARCTTFRQRIYNDTNIDPAFATTRRGNCPQAGAGANLAPLD-GTPTQFDNRYYQDL
                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTGTNGEIRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 TIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 DGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAH 187
                                                                                                                                                                                                                                                                                                                                                                                            CRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLVGGPTWTVPLGRRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 997.5;
Pred. No. 2.1
                                                                from GB/EMBL/DDBJ
                                                                                                                            January 1997
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                                                                                                                                                                                             11-Jun-1999 #text_change
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C;Accession: A91094; ACCESSION: A91094; ACCESSION: A91094; ACCESSION: A91094; ACCESSION: A91094; A01-489, 1980
Eur. J. Biochem. 108, 481-489, 1980
A;Title: Covalent structure of turnip peroxidase 7. Cyanogen A;Title: Covalent structure of turnip s
                                                                                                                                     R.Welinder, K.G.

R.Welinder, K.G.

R.Welinder, K.G.

Bur. J. Biochem. 151, 497-504, 1985

Eur. J. Biochem. 151, 497-504, 
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C; Superfamily: peroxidase
C; Keywords: heme; iron; metalloprotein; oxidor
C; Keywords: heme; iron; metalloprotein; oxidor
E; 37-118/Disulfide bonds: #status predicted
E; 64/Active site: Arg #status predicted
E; 68, 196/Binding site: heme iron (His) (axial
E; 70-75/Disulfide bonds: #status predicted
E; 203-228/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: subspecies C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Welinder, K.G.; Mazza, G.
Eur. J. Biochem. 73, 353-358, 1977
Eur. J. Biochem. 73, 353-358, 1977
A; Title: Amino-acid sequences of heme-linked, histidine-containing peptides A; Reference number: A91246; MUID:77138218; PMID:849740
A; Accession: A91246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Brassica rapa (turn1p)
C;Date: 31-Oct-1980 #sequence_revision 23-Oct-1981 #text_change 03-Mar-2000
C;Accession: A91094; A91246; B23116; PN0612; A00503
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                                                 A; Molecule
                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                      A; Note: these two histidine-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 32-65; 161-175 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the protein shown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-296 <MAZ>
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type: protein : 'Z', 2-296 <W
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peroxidase (EC 1.11.1.7) - radish
C:Species: Raphanus sativus (radis
C:Date: 16-Jul-1999 #sequence_revi
C:Accession: T10252
R:Park, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: peroxidase
C;Superfamily: peroxidase
C;Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase;
F;L/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11-91,44-49,97-292,176-201/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: PN0612; MUID:93384622; PMID:8396932
A;Accession: PN0612
A;Molecule type: protein
A;Residues: 'Z',2-32,'AG',35-88,'D',90-156,'K',158-296 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Dlehn, S.H.; Burkhart, W.; Graham, J.S.
Biochem. Biophys. Res. Commun. 195, 928-934, 1993
Biochem. Brighys. Res. Commun. 195, 928-934, 1993
A;Title: Purification and partial amino acid sequence of wound-inducible,
A;Reference number: PN0612; MUID:93384622; PMID:8396932
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                                                                                                                                                                                                        C;Superfamily: peroxidase C;Keywords: chromoprotein; glycoprotein; heme; iron; oxidoreductase
                                                                                                                                                                                                                                                               A; Gene: prxk1
A; Introns: 68/3; 131/3; 186/3
                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-315 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T10252
                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z16998
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                   밁
                                                                                                                                                                                                                                                                                                                    A; Experimental source: cultivar Handsome
                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X91172
                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                         Query Match
Best Local S
Matches 184
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                                   GCDGSILLD---AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDG 126
                                                                                                        ARVYNETNINAAFATLRQRSCPRAAGSGDANLAPLDINSATSFDNSYFKNLMAQRGLLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVRFDTAYFTNLLSRRGLFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGRRDAKTASQAAANSNIPAPSMSLSQLISSFSAVGLSTRDMVALSGAHTIGQSRCVNFR
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                   GCDGSILLDDTSFTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAIAARDS
                                                                                      VIVITLLLQGGEAQLTTNFYSTSCPNLLSTVKSGVKSAVSSQPRMGASILRLFFHDCFVN
                                                                                                                                                           184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182;
                                                                                                                                                       h 58.3%; Score 935; DB 2; Similarity 59.9%; Pred. No. 2.5e-68; 84; Conservative 44; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 61.8
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sativus (radish)
#sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                          Length 315;
                                                                                                                                                           Indels
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C;Species: Oryza sativa (rice)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S22087
R;Reimmann, C.; Ringli, C.; Dudler, R.
submitted to the EMBL Data Library, June 1992
A;Description: cDNA cloning and sequence analysis of a pathogen-
A;Reference number: S22087
A;Accession: S22087
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S22087
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C;Superfamily: peroxidase
C;Keywords: chromoprotein: heme; iron; metalloprotein;
F;36-111/Disulfide bonds: #status predicted
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A; Residues: 1-317 <REI>
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peroxidase
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   118 ILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSP
                                                                                                                       296 VLTGTAGQIRRNCRVVNS 313
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                                                                                                                                                                                                                                                                                                                                                                           LLRLHFHDCFVQGCDASVLL-SGQEQNAGPNVGSLRGFSVIDNAKARVEAICNQTVSCAD
                                                                                                                                                                                                                                                                                                                                                                                            LLRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCAD
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                                                                                                                                                                                                                               TDMVALSGAHTIGQAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAFVDTTT
                                                                                                                                                           PNAFDNAYYSNLLSNKGLLHSDQYLFNGGSADNTVRNFASNAAAFSSAFTTAMVKMGNIS
                                                                                                                                                                                            PVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVG
                                                                                                                                                                                                                                                                                                    186;
(E)
1.11.1.7) - rice
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Pred. No. 9.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 317
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Gaps

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125 121 65 65

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R; Buffard, D.; Breda, C.; van Huystee, R.B.; Asemota, O.; Pierre, M.; Dang Ha, D.B.; Est Proc. Natl. Acad. Sci. U.S.A. 87, 8874-8878, 1990
A; Title: Molecular cloning of complementary DNAs encoding two cationic peroxidases from A. Reference number: A38265, MUID:91062381; PMID:2247460
A; Status: preliminary A. Molecule type: mRNA A. Residues: 1-316 <BUP A.; Cross-references: GB:M37636
C; Superfamily: peroxidase (Superfamily: peroxidase (Super
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Experimental source: cv. Nipponbare, root C/Superfamily: peroxidase C/Superfamily: peroxidase C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;34-109/Disulfide bonds: #status predicted F:61/Active site: Arg #status predicted F:65,187/Binding site: heme iron (His) (axial ligands) #status predicted F:67-72/Disulfide bonds: #status predicted F:115-310/Disulfide bonds: #status predicted F:115-310/Disulfide bonds: #status predicted F:115-310/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peroxidase (EC 1.11.1.7) precursor, cationic (clone PNCI) - peanut (;Species: Arzchis hypogaea (peanut) C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 04-Mar-2000 C;Accession: A38265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Oryza sativa (rice)
C; Date: 23-Apr-1999 #sequence_revisi
C; Accession: T03929
R; HOri, M.; Sasaki, T.; Minobe, Y.
submitted to the EMBL Data Library,
A; Description: Peroxidase from rice
         F;119-312/Disulfide bonds: #status
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A;Molecule type: mRNA
A;Residues: 1-314 <HOR>
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Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGOIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPVRF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPTLMQCLVAVSLLSCVAHAQLSPTEYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSAYYTNLLSNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSYSIMILIVAAAMAS-AASAQISATFYDTSCPNALSTIKSAVTAAVNSEPRNGASIVRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALSGAHTIGQAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFHDCFVQGCDASVLL-SGQEQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAV
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Pred. No. 1.3e-67;
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C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; pyroglutamic a
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-316/Product: peroxidase 1 #status predicted <MAT>
F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *#status predicted
F:52-112/Disulfide bonds: #status predicted
F:53/Active site: Arg #status predicted
F:63,190/Binding site: heme iron (His) (axial ligands) #status predicted
F:65-70/Disulfide bonds: #status predicted
F:65-70/Disulfide bonds: #status predicted
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues; 1-316 < BAG>
A; Cross-references: EMBL: x85227; NID: 9732969; PIDN: CAA59484.1; PID: 9732970
A; Cross-references: EMBL: x85227; NID: 9732969; PIDN: CAA59484.1; PID: 9732970
A; Cross-references: EMBL: x85227; NID: 9732969; PIDN: CAA59484.1; PID: 9732970
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A; Cross-references: EMBL: x85227; PID: 9732969; PIDN: CAA59484.1; PID: 9732970
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R;Title: Molecular cloning and expression analysis of peroxidase genes from wheat. A;Reference number: S61405; MUID:96128008; PMID:8541492
A;Accession: S61405
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117 DILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISI.FGRQGLS
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                                                                                                                                        61 LFFHDCFVQGCDGSILL-DAG---GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCA 116
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                                                                                                                                                                                                                                                                                                                   1 MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLR 60
                                                                                                                                                                                                                                                                   1 MASASRLGLVVLVAMAS-AASAQLSSTFYDTSCPNALATIKAGVTTAVQNEARMGASLVR 59
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                                                                                   LHFHDCFVDGCDGSVLLADTGSFIGEQGAAPNNNSIRGMNVIDNIKTQVEAVCKQTVSCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLSGAHTIGQAQCTAFRTRIYNESNIDPTYAKSLQANCPSVGGDTNLSPFDVTTPNKFDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                              185;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 58.
85; Conservative
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58.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 915.5;
Pred. No. 9.5e
41; Mismatches
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Pred. No. 2.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 38
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04-Mar-2000

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wheat

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C;Genetics: 70/3; 134/3
R;Introns: 70/3; 134/3
C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; pyroglutamic if;1-23/Domain: signal sequence *status predicted <SIG>F;1-23/Domain: signal sequence *status predicted <MANT>
F;24/Hodified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predicted
F;34-114/Disulfide bonds: *status predicted
F;65,192/Binding site: heme iron (His) (axial ligands) *status predicted
F;67-72/Disulfide bonds: *status predicted
F;100-315/Disulfide bonds: *status predicted
F;199-224/Disulfide bonds: *status predicted
F;199-224/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-319 <BAG>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S61408; S53110
R;Baga, M.; Chibbar, R.N.; Kartha, K.K.
Plant Mol. Biol. 29, 647-662, 1995
A;Title: Molecular cloning and expression analysis of peroxidase A;Reference number: S61405; MUID:96128008; PMID:8541492
A;Accession: S61408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase (EC 1.11.1.7) 4 precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 27-Apr-1996 #sequence_revision 26-J C;Accession: $61408; $53110
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A;Note: exon/intron junctions have been confirmed by mRNA sequencing
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                                                                                              245
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                                                                                                                                                                                                                  180 MTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPV 237
                                                                                                                                                                                                                                                                 125
                   305
                                                                                                                                                                                                                                                                                                   120 ALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTGTAGQIRRNCRVVNS
                                                                                                                                                                                                                                                                                                                                                                 HDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADIL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTGTQGQIRLVCSKVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQCLVAVSLLSCVA---HAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFF 63
                                                                                                                     RPDTAYFTNILLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVL 297
                                                                                                                                                                               MVALSGAHTIGQAQCQNFRDRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPN
                                                                                                                                                                                                                                                               HDCFVQGCDASILLSDTATFTGEQGAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADIL
                                                                                                                                                                                                                                                                                                                                                                                                                           MASSLSVLLLLCLAAPSSAQLSPRFYARSCPRAQAIIRRGVAAAVRSERRMGASLLRLHF
                                                         TGTAGQIRRNCRVVN 312
                                                                                                AFDNAYYRNLMSQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRDFRAAMVSMGNISPL
                   TGTQGQVRLSCSRVN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.8%; Score 895.5; DB 57.5%; Pred. No. 4e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
. B56555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;65/Active site: Arg #status predicted
F;69,196/Binding site: heme iron (HLS) (axial ligands)
F;71-76/Disulfide bonds: #status predicted
F;124-318/Disulfide bonds: #status predicted
F;203-229/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: Chromoprotein; heme; iron; metalloprotein; F;1-27/Domain: signal sequence *status predicted <SIG>F;38-118/Disulfide bonds: *status predicted F;38-118/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M74103; NID:9170202
A;Experimental source: protoplasts
A;Experimental source: protoplasts
A;Note: sequence extracted from NCBI backbone (NCBIN:118061, NCBIP:118062)
C;Superfamily: peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-322 <CRI>
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                                                                                                                                                              peroxidase (EC 1.11.1.7) 2 precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change C;Accession: S61406; S53108 R;Baga, M; Chibbar, R.N.; Kartha, K.K. plant Mol. Biol. 29, 647-662, 1995
                                                                                                                                                                                                                                                                                        RESULT
S61406
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A;Cross-references: EMBL:X85228; NID:g732971; PIDN:CAA59485.1; PID:g732972 A;Note: exon/intron junctions have been confirmed by mRNA sequencing C;Genetics:
                                          A; Molecule type: DNA
A; Residues: 1-314 <BAG>
A; Cross-references: EMB
                                                                                                    A;Title: Molecular cloning and expression analysis of peroxidase A;Reference number: S61405; MUID:96128008; PMID:8541492 A;Accession: S61406
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASPT----LMQCLVAVSLLSCV-AHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVSCADILALAARDGINLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLIRLHFHDCFVQGCDASILLDETPSIESEKTALPNLGSARGFGIIEDAKREVEKICPG
                                                                                                                                                                                                                                                                                                                                                                                                            MGNVGVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROGLSPRDMTALSGAHTIGQARCTTFRGRIYGD-TDINASFAALROQTCPRSGGDGNLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGDNLNSVRGFEVIDTIKRNVEAACPG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDLVTPNQFDNNYFKNLIQKKGLLQSDQVLFNGGSTDNIVSEYSNSARAFSSDFAAMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.40
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 894; DB 2;
Pred. No. 5.4e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.; Parmentier, Y.; Jamet, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxidoreductase
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C;Superfamily: peroxidase
C;Reywords: chromoprotein; glycoprotein; heme; iron; me
F;1-23/Domain: signal sequence #status predicted <SIC>
F;24-312/Product: peroxidase #status predicted <MAT>
F;34-107/Disulfide bonds: #status predicted
F;61/Active site: Arg #status predicted
F;65,185/Binding site: heme iron (His) (axial ligands)
F;67-70/Disulfide bonds: #status predicted
F;113-307/Disulfide bonds: #status predicted
F;113-307/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
S13325
                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-312 <HER>
                                                                                                                                                                                                                                                                                                                                    R;Hertlg, C.; Rebmann, G.; Bull, J.; Mauch, F.; Dudler, R.
Plant Mol. Biol. 16, 171-174, 1991
A;Title: Sequence and tissue-specific expression of a putative peroxidase gene from whee A;Reference number: S13325; MUID:91363838; PMID:1653627
A;Accession: S13325
                                                                                                                                                                                                                                                                                                                                                                                                  peroxidase (EC 1.11.1.7) precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S1325 R;Hertig, C.; Rebmann, G.; Bull, J.; Mauch, F.; Dudler, R.
                                                                                                                                                                                                                                         A; Introns: 68/3; 127/3
                                                                                                                                                                                                                                                                     A; Cross-references: GB: X53675;
                                                                                                                                                                                                                                                                                                                     A; Status: not compared with
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C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreduc:
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-314/Product: peroxidase 2 #status predicted <MAT>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature F;34-109/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;115-309/Disulfide bonds: #status predicted
        Matches 173;
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
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les 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDWTALSGAHTI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCDASVLL-SGMBQNAGPNVGSLRGFGVIDNIKTQLESICKQTVSCADILTVAARDSVVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVVLVALATAASGQLSSTFYDTSCPRALATIKSGVAAAVSSDPRMGASLLRLHFHDCFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVNS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOKGLLHSDOVLENNDTTDNTVRNFASNAAAFSSAFTTAMIKMGNIAPLTGTQGQIRLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKAQCSNFRTRIYGGDTNINTAFATSLKANCPQSGGNTNLENLDTTTPNAFDNAYYTNLL
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                         Similarity
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          Conservative
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                    53.0%;
55.1%;
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                                                                                                                                                                                                                                                                                                                   conceptual translation
                                                                                                                                                                                                                                                              GB:S54871; NID:g21830; PIDN:CAA37713.1;
        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
     Score 849.5;
Pred. No. 2.1e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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                  1.1e-61
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                                    ٧.
                                                                                                                                                                                                metalloprotein; oxidoreductase
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     Indels
                                    Length
                                                                                                                    #status
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                                    312;
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   Gaps
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F:58/Active site: Arg #status predicted
F:62,189/Binding site: heme iron (His) (axial ligands) #status
F:64-69/Disulfide bonds: #status predicted
F:117-311/Disulfide bonds: #status predicted
F:196-221/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: peroxidase C; Keywords: heme; iron; metalloprotein; oxid F; 31-111/Disulfide bonds: #status predicted F; 31-111/Disulfide B; 31-111/Disulfid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T09165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z16599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable peroxidase (EC 1.11.1.7) (clone PC18) - spinach C;Species: Spinacia oleracea (spinach) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_C;Accession: T09165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: prxr5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: subspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type:
A; Residues: 1-315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T09165
                                                                                        Matches
                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                              196-221/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TALSGAHTIGQARCTTFRGRIY-GDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
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LSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQGCDGSI 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNAYYTNLLSQKGLLHSDQVLFNNETTDNTVRNFASNAAAFSSAFTTAMIKMGNIAPLTG
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                                                                                        170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAARDSVVALGGPSWTVPLGRRDSTTASASLANSDLPGPSSSRSQLEAAFLKKNINTVDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-315 <SIM>
                                                                                                                       Similarity
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: Y10466
                                                                                                                       56.3%;
                                                                            42;
                                                                                Score 846.5;
Pred. No. 3.7e
42; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              oxidoreductase
                                                                                                                   .7e-61;
                                                                                                                                                             В
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                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                      predicted
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                                                                        Gaps
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252 GLFHSDQELFNGGSQ-DALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNCRV

ARCTSFRPHIHNDTNINAAFAKSLQKKCPQSGNGKVLQPLDYQTKFRFDDKYYQNLLVKK

253

132 134 192 194

74

76

14 LSUTVNGQLSPNFYSSTCPNALRIVKQGIAKRIKKEARVGASILRLHFHDCFVNGCDGSI 73

LLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLG 131

LLDDTSTFRGEKTAIPNKNSVRGFKAVDSIKASLEKACPGVVSCADILAIASRDAVVQYG 133

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Rebmann, G.; Hertig, C.; Bull, J.; Mauch, F.; Dudler, R.
Tant Mol. Biol. 16, 329-331, 1991
;Fitle: Cloning and sequencing of cDNAs encoding a pathogen-induced putative peroxidase;Reference number: S13375; MUID:91370874; PMID:1893103
;Accession: S13375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: mRNA;Residues: 1-312 <REB>;Residues: 1-312 <REB>
;Residues: 1-312 <REB>
;Cross-references: GB:X56011; GB:S55687; NID:g21828; PIDN:CAA39486.1; PID:g21829;
;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 135-Tyr;Superfamily: peroxidase
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase 1-22/Domain: signal sequence #status predicted <SIG>23-312/Product: peroxidase #status predicted <WAT>33-108/Disulfide bonds: #status predicted
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Q9pjy2 P82281 O334/9

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pseudomonas thermotoga

P20013 Q92879 P28659 P36852 O59651 P50622 P04693 O28045

phanerochae escherichia archaeoglob

haloarcula

homo sapien mus musculu human adeno

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                          PERX_WHEAT
APX1_PEA
APX1_ARATH
PEM4_PHACH
PEM1_PHACH
LIG_PHURA
PER_ARTRA
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PER1_LYCES
PERX_SOLTU
PERX_LUPPO
PER2_HORVU
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                                   Q02200 nicotiana s
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p80679 armoracia r
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p15232 armoracia r
p17180 armoracia r
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p37834 oryza sativ
p20144 lycopersico
p12437 solanum tul
p15940 triticum ae
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p002567 phanerochae
p20010 phlebia rad
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CARBOHYD
                                                              Multigene
MOD_RES
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ACT_SITE
METAL
                                                                                                                   PROSITE;
                                                                                                                                                                                              P00434;
21-JUL-1986 (Rel. 20, Created)
21-JUL-1984 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxidase P7 (EC 1.11.1.7).
Brassica rapa (Turnip)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID-51350;
                                                                                                                                            SUBFAMILY.

PIR; A00503; OPNB7.

PIR; B23116; B23116.

HSSP; P22195; ISCH.

InterPro; IPR002016; Peroxidase.

Pfam; PF00141; peroxidase; I.
                                                                                                                                                                                                                                                                                                                     Mazza G., Welinder K.G.;
"Covalent structure of turnip peroxidase 7. Cyanogen bromide fragments, complete structure and comparison to horseradish peroxidase C.";
                                                                                                                                                                                                                                                                                  SEQUENCE OF 32-65 AND 161-175.
MEDLINE=77138218; PubMed=849740;
                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Blanc dur d'hiver;
MEDLINE=81003872; PubMed=7408864;
                                                                                                             Oxidoreductase;
                                                                                                                                       PRINTS; PR00458; PEROXIDASE
                                                                                                                                                                                                                                                                          Welinder K.G., Mazza G.;
                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 108:481-489(1980).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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           ME.
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CUG1_HUMAN
CUG1_MOUSE
HEX_ADE08
CATA_HALMA
LIG6_PHACH
TYRE_ECOLI
THSA_ARCFU
PMPB_CHLMU
TL29_ARATH
ICEV_PSESY
ILVD_THEMA
           N-LINKED (GLCNAC. ..).
53C9CCE59B2A7937 CRC64;
                                                               PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
DISTAL HISTIDINE (BY SIMILARITY).
IRON (PROTOHEME IX AXIAL LIGAND).
                                                                                                             Peroxidase;
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Result No.

Score

894 849.5 818 736.5 723

129 118.5 112

262 206 197.5 190.5

108.5 107.5 106.5 104.5

713.5
702.5
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684
676.5
640
638
638
650.5
546.5
535.5

Minimum Maximum

DB Bd

seq seq

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of.

Database

and is Pred. Scoring table:

Title: Perfect score:

Sequence:

Run 8

protein

Query Match Best Local

Similarity

58.7%;

Score 942; Pred. No. 3.

Length

296;

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PERL_ARAHY STANDARD,
P22195;
01-AUG-1991 (Rel. 19, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                              Buffard D., Breda C., van Huystee R.B., Asemota Dang Ha D.B., Esnault R.; Buffard Cloning of complementary DNAs encodin peroxidases from cultivated peanut cells."; Proc. Natl. Acad. Sci. U.S.A. 87:8874-8878(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAHY
                                                                                                                  Structure 4:311-321(1996).

-!- FUNCTION: REMOVAL OF H(2)O(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOWN MOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
-!- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(3)O(2) = Oxidized donor + 2 H(3)O(3)OXIDE CONTRACTOR: Binds 1 protoheme IX, 1 iron(III) ion and 2 calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91062381; PubMed-2247460;
                                                                                                                                                                                                           Schuller D.J., Ban N., van Huystee R.B., McPherson A., "The crystal structure of peanut peroxidase.";
                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.7 MEDLINE-96398617; PubMed-88
            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                        REVISION TO 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-3818;
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SIMILARITY: BELONGS
SUBFAMILY.
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PER2_ORYSA P37835;

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RESULT 3
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DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0458; PEROXIDASE_1; 1.
PROSITE; PS004435; PEROXIDASE_2; 1.
Oxidoreductase; Glycoprotein; Peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1SCH; 11-JUL-96.
GlycoSuiteDB; P22195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002016; Peroxidase
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M37636;
                                                                                                                                                                                                                                                                                                                                       CA_BIND
                                                                                                                                                                                                                                                                                                                                                CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family; Signal;
                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                          246
                                                                                                                  126
                              306
                                           302
                                                                                      186
                                                                                                    182
                                                                                                                                122
                                                                                                                                              66
                                                                                                                                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A38265;
1SCH; 1
                                                                                     ALGGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDT
                                                                                                                                                                                  AARDGTNILGGDTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMT
                                                                                                                                             CFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGYVSCADILAL 121
                                                                                                                  GQIRTNCRKTN
                                           GQIRRNCRVVN 312
                                                         AYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTA
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                 316 AA;
                                                                                                                                                                                                                                                                                                                                               53
68
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72
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192
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64
191
23
82
166
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB06183.1;
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166
                                                                                                                                                                                                           57.8%;
58.5%;
                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure
                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                    DISTAL HISTIDINE.
IRON (PROTOHEME IX AXIAL LIGAND).
PYRROLIDOME CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
/FTId=CAR_000185.
                                                                                                                                                                                                            Score 927; DB 1;
Pred. No. 6.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CATIONIC PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                           (VIA CARBONYL OXYGEN).
                                                                                                                                                                                                                                  2CC271F8E8B8C9F0 CRC64;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Iron;
                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                       Heme;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding;
                                                                                                                                                                                                        10;
                                                                                                                                                                                                        Gaps
                                                                                         245
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CARBOHYD
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01-OCT-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LIGHT, DEFENSE RESPONSE TORM WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

-i- CATALYTIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2 H(2) - CATALYTIC BROWN AND AND ADMINISTRATION OF THE CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(2) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY: DONOR + H(2)0(1) = OXIDIZED ON - 2 H(2) - CATALYTIC ACTIVITY - C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00435; PEROXIDASE_1; PROSITE; PS00436; PEROXIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002016; Peroxidase
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hor 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00458;
                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family;
    182
                               182
                                                            122
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                                                                                                                                             62
                                                                                                                                                                                                                                                 Local
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                                                                                                                                  FFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M., Sasaki T.,
                                                       HFHDCFYQGCDASVLL-SGQEQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAV
                                                                                                                                                                                                   ASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
ALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPVRF
                                                                                                                                                                        ASSVSLMLLVAAAMAS-AASAQLSATFYDTSCPNALSTIKSAVTAAVNSEPRMGASLVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D16442; BAA03911.1; P22195; ISCH.
                                                                                                                                                                                                                                    185;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 (Rel. 30,
94 (Rel. 30,
92 (Rel. 41,
94 precursor (
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magnoliophyta;
Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
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24
61
187
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169
203
274
                                                                                                                                                                                                                                                 57.78;
59.18;
                                                                                                                                                                                                                                                                                        32606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
(EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                           PEROXIDASE. .

PYROLIDONE CARBOXYLIC ACID (POTENTIAL).

BY SIMILARITY.

DISTAL HISTIDINE (BY SIMILARITY).

IRON (PROTOHEME IX AXIAL LIGAND) (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .

N-LINKED (GLCNAC. .

N-LINKED (GLCNAC. .

3; 232C874730D6C7FB (
                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peroxidase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liliopsida; Poales;
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                              926;
                                                                                                                                                                                                                                                                                                    GLCNAC...
GLCNAC...
GLCNAC...
GLCNAC...
GLCNAC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
                                                                                                                                                                                                                                             DB 1;
.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                          Length 314;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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L outstation -
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   241
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PERX_NICSY
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DISULFID DISULFID
                                                         METAL
                                                                                                                               CHAIN
                                                                                                                                           SIGNAL
                                                                                                                MOD_RES
                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana sylvestris be replicational activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Criqui M.-C., Pless
Jamet E., Fleck J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lignin forming anionic peroxidase precursor (EC 1.11. Nicotiana sylvestris (Wood tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                 Oxidoreductase;
                                                                                                                                                                                                                                                                          Pfam; PF00141; peroxidase;
                                                                                                                                                                                                                                                                                                              EMBL; M74103; AAA34050.1;
HSSP; P22195; 1SCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93041285;
Criqui M - ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of genes e
Nicotiana sylvestris before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERX_NICSY
                                                                                                                                                                                                                                                                                               InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + COFACTOR: Binds I protoheme IX and I iron(III) ion.
TISSUE SPECIFICITY: MESOPHYLL PROTOPLASTS AND TO A MUCH EXTENT, ROOTS AND GERMINATING SEEDS.
DEVELOPMENTAL STAGE: BEFORE RE-INITIATION OF THE DNA REJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h. Dev. 38:121-132(1992).

FUNCTION: THIS ENZYME PLAYS AN INTEGRAL ROLE IN SECONDA WALL BIOSYNTHESIS BY THE POLYMERIZATION OF CINNAMYL ALC INTO LICKIN AND BY FORMING RIGID CROSS-LINKS BETWEEN CE PECTIN, HYDROXY-PROLINE-RICH GLYCOPROTEINS, AND LIGNIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTAYFTNILSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTG
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T "Sequence and tissue-specific expression of a putativ

gene from wheat (Triticum aestivum L.).";

L Plant Mol. Biol. 16:171-174(1991).

-!- FUNCTION: INVOLVED IN DEFENSE RESPONSE TO POWDERY

-!- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized du

-!- COFACTOR: Binds 1 protoheme IX and 1 iron(III) iou

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUE SPECIFICITY: ROOT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID CARBOHYD
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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yta; Liliopsida; Poales; Poaceae; Pooidea
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Best Local S
Matches 173
                                SEQUENCE FROM N.A.

STRAIN-CV. Pallas / P-01; TISSUE-Seedling leaf;
Thordal-Christensen H., Brandt J., Cho B.H., Rasm
Gregersen P.L., Smedegaard-Petersen V., Collinge
"CDNA cloning and characterization of two barley
transcripts induced differentially by the powdery
Erysiphe graminis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
ACT_SITE
ACT_SITE
Erysiphe graminis.",
Physiol. Mol. Plant Pathol.
-!- FUNCTION: INVOLVED IN DE
-!- CATALYTIC ACTIVITY: Dono
                                                                                                                              Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
Triticeae; Hordeum.
                                                                                                                                                                       PERI_HORVU STANDARD; PRT; 3
P27337;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peroxidase 1 precursor (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
                                                                                                                                                                                                                                        HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Glycoprotein; Peroxidase; Multigene family; Signal.
                                                                                                                    NCBI_TaxID=4513;
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70 B
307 B
218 B
262 N
32381 MW;
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55.1%;
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BY SIMILARITY.
DISTAL HISTIDINE (BY SIMILARITY).
DISTAL HISTIDINE (IX AXIAL LIGAND) (B SIMILARITY).
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FF468A33F3DC68F7
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on update)
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    TO POWDERY MELDEW oxidized donor + :
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                                            e D.B.;
y peroxidase
ry mildew fungus
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    FUNGUS
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Best Local :
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PERX_ARMRU STANDARD P80679; 01-OCT-1996 (Rel. 34, C 01-OCT-1996 (Rel. 34, L 15-JUN-2002 (Rel. 41, L Peroxidase (EC 1.11.1.7 Armoracia rusticana (HC
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HSSP; P22195; ISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00435; PEROXIDASE_1; 1. PROSITE; PS00436; PEROXIDASE_2; 1. Oxidoreductase; Glycoprotein; Pero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                           ARMRU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion. SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
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                                                                                                                     KTGTQGQIRLSCSRVNS
                                                                                                                                        LTGTAGQIRRNCRVVNS
                                                                                                                                                              NTFDNAYYTNLMSQKGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSSFTTAMIKMGNIAP
                                                                                                                                                                         VRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGV
                                                                                                                                                                                                        MVALSGAHTIGQAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGSLANLDTTTA
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  (Horseradish) (Armoracia laphatifolia).
           , Last sequence up Last annotation 1.7).
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4; Mismatches
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Pred. No. 3.1e-58
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BY SIMILARITY.
DISTAL HISTIDINE
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                                 update)
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                       update)
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CARBOHYD
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mitted (AUG-1996) to the SWISS-PROT data bank.
FUNCTION: REMOVAL OF H(2)O(2), OXIDATION OF TOXIC REDUCT?
BIOSYNTHESIS AND DEGRADATION OF LIGHIN, DEFENSE RESPONSE
WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT E
DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
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                                                                         KVD
                                                                                                                                                                                                                                                     LGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQARCTTFR 198
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                                                                                                                                                                                                                                                                                                                                                                                          QLNATFYSGTCPNASAIVRSTIQQAFQSDTRIGASLIRLHFHDCFVDGCDASILLDDSGS
                                      VVN 312
                                                                                                                                                      NRLFNFSGTNGPDPTLNSTLLSSLQQLCPQNGSASTITNLDLSTPDAFDNNYFANLQSNN
                                                                                                                                                                                             GRIYG----
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2 42 B
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PEROXIDASE_2;
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BY SIMILARITY.
PYRROLIDONE CARBOXYLIC P
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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Pred. No. 9.6e
18; Mismatches
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les 95;
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RESULT 8
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Best Local
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CARBOHYD
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PROSITE: PS00436; PEROXIDASE_2; 1.
Ovidoroductase: Peroxidase; Iron; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Wange by and for commodified and this statement is not removed. The substitutions as its content is in modified and this statement is not removed. The substitutions are substitutions as its content is not removed.
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01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
11-JUN-2002 (Rel. 11, Last annotation update)
11-JUN-2002 (Rel. 12, Last sequence update)
11-JUN-2002 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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HSSP; P00433; 2ATJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Lagrimini L.M., Bur molecular cloning
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                                                                                                                                                                                                                                                                AHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQGCDGSILLDA
VPLGRRDSTTASASLANSNPPPPTASLGTLISLEGROGLSPRDMTALSGAHTIGQARCTT 196
                                                                                                DGTQTEKDAPANVGA-GGFDIVDDIKTALENVCPGVVSCADILALASEIGVVLAKGPSWQ 138
                                                                                                                                                                                                                               SNAQLSATEYDTTCPNVTSIVRGVMDQRQRTDARAGAKIIRLHFHDCFVNGCDGSILLDT
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117
196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEROXIDASE.
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48.7%;
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PYROLIDONE CARBOXYLIC ACID.
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DISTAL HISTIDINE (BY SIMILARITY).
IRON (PROTOHEME IX AXIAL LIGAND) (B'SIMILARITY).
BY SIMILARITY.
OFICIARCO...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Pred. No. 1.2e
50; Mismatches
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L.2e-50;
nes 93;
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PERC_ARMRU
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X MEDLINE-88225087; PUDMed=3371352;

A Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takano M., Yamada Y., Okada H.;

T "Structure of the horseradish peroxidase isozyme C genes.";

LEUR. J. Biochem. 173:681-687(1988).

C -!- FUNCTION: REMOVAL OF H(2)(0(2)) OXIDATION OF TOXIC REDUCTANTS

C -!- FUNCTION: REMOVAL OF H(2)(0(2)) OXIDATION OF TOXIC REDUCTANTS

C BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOME

WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE

C DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

C -!- CATALYTIC ACTIVITY: DODOR + H(2)(2) - OXIDATED

C -!- CATALYTIC ACTIVITY: DODOR + H(2)(2) - OXIDATED

C -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE

STRINGARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
   DISULFID DISULFID
                                             ACT_SITE
ACT_SITE
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armoracia rusticana (Horseradish) (Armoracia laphatifolia). Eukaryota; Viridiplantae; Streptophyta; Emycophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Armoracia. NCBI_TaxID=3704;
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PIR; S00627; S00627.
HSSP; P00433; 2ATJ.
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxidase CIC precursor (EC 1.11.1.7) (Fragment).
                                                                                                                                          SIGNAL
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                                                                                                                                                                         family; Signal.
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179
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DISTAL HISTIDINE (
IRON (PROTOHEME I)
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                          PYRROLIDONE
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RESULT 10
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190433;
21-JUL-1986 (Rel. 01, Created)
11-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
19-JUN-2002 (Rel. 41, Last annotation update)
19-PROXIDASE CIA precursor (EC 1.11.1.7).
19-PRXCIA OR HPRCI.
19-PRXCIA OR HPRCI.
19-PRXCIA OR HPRCI.
19-PRXCIA TUSTICANIA (HOTSETAGISH) (Armoracia laphatifolia).
19-PRXCIA Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
19-PRXCIA Magnollophyta; endicotyledons; core endicots; Rosida eurosids II, Brassicales; Brassicaceae; Armoracia.
MEDLINE=98069652; PubMed=9406554; Gajhede M., Schuller D.J., Henriksen A., Smit "Crystal structure of horseradish peroxidase Nat. Struct. Biol. 4:1032-1038(1997).
                                                                                                                                                [2]
SEQUENCE OF 31-338.
SEQUENCE OF 31-338.
                                                                                                                                                                                                           Fujiyama K., Takemura H., Shibayama S., K
Shinmyo A., Takano M., Yamada Y., Okada H
"Structure of the horseradish peroxidase
Eur. J. Biochem. 173:681-687(1988).
                                                                                                                                              MEDLINE=77068850;
Welinder K.G.;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                 X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
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between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The burden Bioinformatics Institutes to mon-profit institutions as long a
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98272679; PubMed=9609699;
Henriksen A., Schuller D.J., Meno
entities requires a license agreement (S or send an email to license@isb-sib.ch).
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- SUBUNIT: MONOMER.
- SIMILARITY: BELOW
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                                                                                entry is copyright. It is produced through iss Institute of Bioinformatics and the EM
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PIR; A00502; OPRHC.
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PDB; 1ATJ; 04-FEB-98.
PDB; 2ATJ; 28-JAN-98.
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                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K., Shinmyo A., Takano M., Yamada Y., Okada H.;

Shinmyo A., Takano M., Yamada Y., Okada H.;

Structure of the horseradish peroxidase isozyme C genes.";

Eur. J. Biochem. 173:681-687(1988).

-1- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LICONIN, DEFENDE RESPONSE TOWARD WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEFENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

-1- CATALYTIC ACTIVITY: DONOT + H(2)0(2) - OXIDIZED donor + 2 H(2)0.

-1- COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

-1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE SUBFAMILY.
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Armoracia rusticana (Horseradish) (Armoracia laphatifolia).

Armoracia rusticana (Horseradish) (Armoracia laphatifolia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid

Spermatophyta; Brassicales; Brassicaceae; Armoracia.
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P15232;
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01-APR-1990 (Rel. 14, Last sequence upd
15-JUN-2002 (Rel. 41, Last annotation u
Peroxidase CIB precursor (EC 1.11.1.7).
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Best Local
                                                                                                                                     PERC_ARATH STANDARD; PRT; 35/
P24101;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence updated)
15-JUN-2002 (Rel. 41, Last annotation upon the sequence of t
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SEQUENCE FROM N.A. MEDLINE=91200671;
                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
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PROSITE; PS00436; PEROXIDASE_2; 1.
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Pred. No. 5.8e
88; Mismatches
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SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                            ion update)
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RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Conrad A., Hornischer K., Kauer G., Loehnert T. H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Mayer Y., Rizzo M., Walts A., Utterback T., Fijlic Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujlic Y., Shea T.P.,

RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,

RA Pal S., Militscher J., Sellers P., Gill JE., Feldblyum T.V.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Klyokawa C., Kohara M., Matsunoto M., Muraki A.,

Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wadda T.,

Wa Matanabe A., Yanada M., Yasuda M., Tabata S.,

RA Matanabe A., Yanada M., Yasuda M., Tabata S.,

RA Matanabe A., Yanada M., Yasuda M., Tabata S.,
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                                                                 CHAIN
ACT_SITE
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                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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-1: FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANT BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TO WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
-1: CATALTYIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2:
-1: COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.
-1: TISSUE SPECIFICITY: ROOTS.
-1: SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
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Takano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M58380; AAA32849.1;
EMBL; AL132967; CAB61999.1
PIR; JU0457; JU0457.
HSSP; P00433; 2ATJ.
                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00141; peroxidase;
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                                                                                                                                                                                                                                                                                                                                            PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                          PS00435; PEROXIDASE_1; 1. PS00436; PEROXIDASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                              IPR002016; Peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Columbia;
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CAB61999.1; -.
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NEUTRAL PEROXIDASE C.
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DISTAL HISTIDINE (BY SIMILARITY).
IRON (PROTOHEME IX AXIAL LIGAND).
BY SIMILARITY.
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ESPONSE TOWARD
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STRAIN-CV. Columb: MEDLINE-20083487;
                                                                          Duroux L., Welinder K.G.; "Structural diversity and transcription of Arabidopsis thaliana.";
                                                                                                                                                                 "Nucleotide sequences of Arabidopsis thaliana."; Gene 98:237-241(1991).
                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               P24102; 080913;
01-MAR-1992 (Re
                               SEQUENCE FROM N.A
                                                                                                                                                                                                               Intapruk C., Higashimura Takano M.;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=91200671;
                                                                                                                                                                                                                                                                                                                                                   PRXEA OR AT2G38380 OR T19C21.13.
Arabidopsis thaliana (Mouse-ear cress).
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Pred. No. 5.
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Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

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Best Local :
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EMBL; AF452388; AAC40852.1; -.
EMBL; AC04683; AAC28766.1; -.
EMBL; AY059106; AAL15212.1; -.
EMBL; AY059106; AAL15212.1; -.
EMBL; AY035033; AAK59538.1; -.
FIR; JY00458; JY00458
HSSP; P00433; ZATJ.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; Peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE.2; 1.
Oxidoreductase; Glycoprotein; Peroxidase; Ir
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"Sequence and analysis of chromosome 2
thaliana.";
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     SPTLMQCLVAVSLLSCV-----
                                                                               Similarity
                                                                                                                                                              Conservative
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71
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1173
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                                                     47;
-AHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGA 56
                                                                                                                                                   BASIC PEROXIDASE E.
BY SIMILARITY.
DISTAL HESTIDINE (BY:
IRON (PROTOHEME IX AX:
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (G
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RESPONSE TOWARD
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                         EMBL; D90116; BAA14144.1; -.

PIR; JH0150; JH0150.

HSSP; P00433; ZATJ.

InterPro; IPR002016; Peroxidase.

Pfam; PF00141; peroxidase; 1.

PRINTS; PR00458; PEROXIDASE_1; 1.

PROSITE; PS00435; PEROXIDASE_2; 1.

Oxidoreductase; Glycoprotein; Peroxi
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01-AUG-1990
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                               genes.
Gene 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armoracia rusticana (Horseradish) (Armoracia laphatifolia).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Armoracia.
             Oxidoreductase;
Multigene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLLNE-90323613; PubMed-2373366;
Fujlyama K., Takemura H., Shinmyo
"Genomic DNA structure of two new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peroxidase
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CATALYTIC ACTIVITY: Donor + H(2)O(2) = OXIGIZED GONOR + 2 H(2)O. COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

COPACTOR: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEKOXIDASE SIMILARITY:
                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGLS-PRDMTALSGAHTIGQARCTTFRGRIYG------DTDINASFAALRQQTCPRSGG
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             family;
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0 (Rel. 15, Last sequence up)
2 (Rel. 41, Last annotation (EC 1.11.1.7).
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Signal.
                                Peroxidase;
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ARWRU

PER2_ARWRU

P17179;

P17179;

P101-AUG-1990 (Rel. 15, Cre

O1-AUG-1990 (Rel. 15, Lar

15-JUN-2002 (Rel. 41, Lr

14-JUN-2002 (Rel. 41, Lr
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Matches 149;
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90323613; PubMed=2373366;
Fujiyama K., Takemura H., Shinmyo
                                                                                                                                                                                                                                                                                                                       Armoracia rusticana (Horseradish) (Armoracia laphatifolia). 
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache 
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots 
eurosids II; Brassicales; Brassicaceae; Armoracia.
      ++
                                                                                                                                                                        genes.";
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FUNCTION: REMOVAL OF H(2)O(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOWARD WOUNDING AND METRADALISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

CATALYTIC ACTIVITY: DONOT + H(2)O(2) = OXIGLED donor + 2 H(2)O COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restitute the succession of th
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                    NVGVLTGTAGQIRRNCRVVNS
                                                                                                                                                                                  GAHTIGQARCTTFRGRIYG------DTDINASFAALRQQTCPRSGGDGNLAPIDVQTPV
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NLSPSTGKQGEIRLNCRVVNS
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                                                                                                            RFDTAYFTNLLSRRGLFHSDQELFNGGSQDA-----LVRQYSASASLFNADFVAAMIRMG
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3: sp_fungi:*
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5: sp_inverteb
6: sp_nammal:*
7: sp_mhc:*
8: sp_organel:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
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MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRNGASLLR 60	Query Match 80.5%; Best Local Similarity 81.5%; Matches 255; Conservative 2	24 307 PEROXIDASE. 307 AA; 32507 MW; 526B44B3A7C75FA7 CRC64;	d		PRINTS; PR00458; PEROXIDASE.	rncerero; rekoozoro; eeroxidase Pfam; PF00141; peroxidase; 1.	ISCH.	EMBL; U12314; AAA20472.1;	, Botany, Un	"Investigation of peroxidase genes		STRAIN-CV. BILOELA; TISSUE-WOUNDED	N.A.	877.	Spermacophyca; magnoriophyca; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae: Paniceae: Cenchrus	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Cenchrus ciliaris (Buffelgrass) (Pennisetum ciliare)	Peroxidase precursor (EC 1.11.1.7).		TrembLrel. 0	PRELIMINARY;
HAQLSPTFYASS	24	PEROXIDASE.	POTENTIAL	ASE_2; 1.	SE.	xidase.			iversity of	ase genes and					iyta; Lillops	Streptophyt	grass) (Penn	1.11.1.7).	0, Last anno	01, Created)	PRT;
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GASLLR 60	6; Gaps		٠.				25.0	action of	200	on in		D STEMS;			PACC clade;	ophyta;		-			
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Matches 221
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O1.NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bacterial-induced peroxidase precursor (EC 1.11.1.7).
Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
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SEQUENCE
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Pfam; PF00141; peroxidase; 1.

PRINTS; PR00458; PEROXIDASE.

PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.

PROSITE; PS00436; PEROXIDASE_2; 1.

Oxidoreductase; Peroxidase; Signal.
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Assigbetse K., Cuny G., Valette C., Delannoy E., Bresson E.,
Jalloul A., Daniel J.-F., Geiger J.-P., Nicole M.;
"Cloning and Characterization of a Bacterial-Induced Peroxidase-
"Cloning CDNA from Cotton (Accession No. AF155124). (PGR99-129).
Plant Physiol. 121:312-313(1999).
Plant Physiol. 121:312-313(1999).
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STRDLTALSGGHTIGLARCTTFRGRIYNDTNIDANFAATRRANCPASGGDNNLAPLDIQT
                        SPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGGGNLAPIDVQT
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Query Match
Best Local Similarity
Matches 195; Conserv
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                                                                                                                                                                                                                                                                                                                                                               CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00435; PEROXIDASE_1; UNKNOY PROSITE; PS00436; PEROXIDASE_2; 1. PROSITE; PS01331; THYMIDYLATE_KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase;
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Diveristy and conservation of plant peroxidases."; Plant Peroxidase Newsletter 1:4-7(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                         VLTGTAGQIRRNCRVVN 312
|||| |:|||||||
PLTGTQGEIRRNCRVVN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKNLIAKRGLLHSDQELYNGGSQDALVTRYSKSNAAFAKDFVAAIIKMGNISPLTGSSGE
                    FTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQ
                                                                                                                     GTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEAF;
                                                                                                                                                                                                                                                                                                                                                               309 AA;
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(TIEMBLIEL 03, Last sequence upda
(TIEMBLIEL 20, Last annotation up
precursor (EC 1.11.1.7) (Fragment).
                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 3.3e-73;
6; Mismatches 61; 1
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POTENTIAL.
; C6D54D73E1390755 CRC64;
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Best Local S
Matches 197
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065029;
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Eukaryota; Viridiplantae; Streptophyta; Embryc
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Malpighiales; Linaceae; Linum.
NCBI_TaxID-4006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Peroxidase FLXPER4 (EC 1.11.1.7) (Fragment).
PER4
Q9LWM9;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. STORMONT
Omann F., Tyson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. STORMONT CIRRUS; TISSUE-LEAF;
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                                  6WMT60
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                                                                                                               AMSILASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENRMAASILRLHFHDCFVNGC
                                                                                                                                                                                                                                                                 AVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFFHDCFVQGC
                                                                                                                                                          TIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNL
                                                                                                                                                                                   NLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPRDMTALSGAH 187
                                                                                                                                                                                                                               DGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGT 127
                                                                             CRRPN
                                                                                              CRVVN
                                                                                                                                                  TIGQARCTTFRQRIYNDTNIDPAFATTRRGNCPQAGAGANLAPLD-GTPTQFDNRYYQDL
                                                                                                                                                                                                                      DGSLLLDDTATFTGEKNAGPNQNSVRGFDIIDTIKTRVEAACNATVSCADILALAARDGV
                                                                                                                                                                                                                                                                                           197; Conserv
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) (TrEMBLrel.) (TrEMBLrel.)
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                                    PRELIMINARY;
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15,
21,
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Created)
Last sequ
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                           Score 997.5; 1
Pred. No. 1.2e
37; Mismatches
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                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN_1
sequence up
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                                     319
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          update)
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databases.
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Best Local Similarity
Matches 192; Conserv
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Em Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
NCBL_TaxID=4530;
[1]
                      SEQUENCE FROM N.A. STRAIN-COLUMBIA; MEDLINE-98344145; PKaneko T., Kotani HTabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
PROSITE; PS00436; PEROXIDASE_2; 1.
SEQUENCE 319 AA; 33536 MW; 395E1BE20BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0451C06.";
clone:P0451C06.";
Submitted (MAR-2000) to the EMBL/GenBa
Submitted (MAR-2000) to the EMBL/GenBa
EMBL; AP001551; BAA92967.1;
HSSP; P22195; 1SCH.
                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                 eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                            Q9FLC0;
                                                                                                                                                                                                                        Q9FLC0
                                                                                                                                                    AT5G05340
                                                                                                                                                               Peroxidase (Putative peroxidase)
 "Structural
features of
                                                                                                                                                                                                                                                                                                                                                  246
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                                                                                                                                                                                                                                                                                                                           TNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLEGROGLSPRDMTALSGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQIRRNCRVVNS
                                                                                                                                                                                                                                                                                                                                                                          HTVGWARCSTFRTHIYNDTGVNATFASQLRTKSCPTTGGDGNLAPLELQAPNTFDNAYFT
                                                                                                                                                                                                                                                                                                                                                                                      HTIGQARCTTFRGRIYGDTDINASFAA-LRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFT
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analysis of Arabidopsis thaliana the regions of 1,381,565 bp cover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                        PRELIMINARY;
                                  PubMed=9679202;
H., Nakamura Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%;
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Pred.
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No. 2e
                                    Sato
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                                   s.,
   covered by twen:
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                                    Asamizu
                                                                                                                                                                            update)
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               Sequence
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Best Local Sin
Matches 199;
                                                           PRXR4.

Spinacia oleracea (Spinach).

Spinacia oleracea (Spinach).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracneo

Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Chenopodiaceae; Spinacia.
                                                                                                                                     P93548 PRELIMINARY; PRT; 323 AA. P93548; O1-MAY-1997 (TrEMBLrel. 03, Created) O1-MAY-1997 (TrEMBLrel. 03, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Peroxidase precursor (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Chang C.H., Chang E., Dale J.M., Goldsm Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsm Lee J.M., Ondera C.S., Quach H.L., Tang C., Toriumi M., William Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Hamamura Y., Yu G., Yu S., Bowser L., Kamiya A., Karlin-Neur Kawal J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., S., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.
                             TISSUE-LEAF;
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis A.;

"Full Length cDNA of gene At5g05340 (GI:15239075).";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB010692; BAB09977.1;

EMBL; AY065270; AAL38746.1;

HSSP; P22195; ISCH.
  Diveristy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Pfam; PF00141; peroxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                           GRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVSCADILAIAARDSVVALGGPNWNVKVGRRDARTASQAAANSNIPAPTSSLSQLISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASPTLMQCLVAVSLL-----SCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRM
                                                                                                                                                                                                                                                                                                                                                                                 SAVGLSTRDMVALSGAHTIGQSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGDNLNSVRGFEVIDTIKRNVEAACP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASNKLISILVLVVTLLLQGDNNYVVEAQLTTNFYSTSCPNLLSTVQTAVKSAVNSEARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
 conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34215 MW;
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plant
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peroxidases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
3.3e-71;
nes 77;
                                                                                                                                                        update:
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                                                                                                   Tracheophyta;
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STRAIN=CV. SAMSUN NN; TISSUE-TMV-INFECTED LEAF;

(MEDLINE-99418329; PubMed-10490396;

Hiraga S., Ito H., Matsui H., Honma M., Ohashi Y.;

"CDNA sequences for two novel tobacco peroxidase isoe

P. Nos. ABD27752 and ABD27753). (PGR99-109).";

L. Plant Physiol. 120:1205-1205(1999).

R. EMBL; ABD27752; BAAB2306:1; -.

R. HSSP; PS2195; 1SCH.

R. InterPro; IPR002016; Peroxidase.

R. France, PP00141; Peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 197
                                                                                                                                                                               Q9XIV9;
Q1.NOV-1999 (TrEMBLrel. 12, Created)
Q1.NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1.NOV-1999 (TrEMBLrel. 19, Last annotation update)
Q1.DEC-2001 (TrEMBLrel. 19, Last annotation update)
Peroxidase (EC 1.11.1.7).
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Nicot
                                                                                                                                                                        NCBI_TaxID=4097;
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CHAIN
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Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00455; PEROXIDASE_1; UNI
PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Peroxidase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simon P.;
Submitted (JAN-1997) to t
EMBL; Y10465; CAA71491.1;
HSSP; P22195; ISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNL-NSVRGFEVIDTIKRNVEAACPG
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197; Conser
PR00458;
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323 AA;
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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35283 MW;
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Pred. No. 1.
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1.3e-70;
76;
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Best Local
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                                                                                                                                                                                                                                                                                "Identification and molecular characterization of novel peroxidase with structural protein-like properties.";
J. Biol. Chem. 274:26192-26198(1999).
EMBL; AB024439; BAA77389.1; -.
INTERPROTE TRANSP. P22195. ISCH.
INTERPROTE TRANSP. 13CH.
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01-MAY-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
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PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Peroxidase.
SEQUENCE 321 AA; 34369 MW; 9263872E0F92D448 CRC64;
                                                                                                                                                                                         PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
SEQUENCE 318 AA; 33903 MW; 6CD
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99403061; PubMed=10473572;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Scutelkaria. NCBI_TaxID=65409;
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                                                  LMLVLLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASLLRLHFHDCFVN
                                                                  LVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ
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                  GCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARD 125
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S; PR00458; PEROXIDASI
                                                                                                                                       Similarity
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                                                                                                                        Conservative
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                                                                                                                                                                                                                                             PEROXIDASE.
                                                                                                                                       59.28;
59.98;
59.8%; Score 958.5; DB 1 61.5%; Pred. No. 1.8e-69;
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13,
19,
                                                                                                                      44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Last annotation update)
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Pred. No. 8.4e-69;
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                                                                                                                                                                                         6CDD0DA3FE470C83 CRC64;
                                                                                                                      Mismatches
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                                                                                                                      75;
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RP SEQUENCE FROM N.A.

CSTRAIN-CV. IRBBLO; TISSUE-LEAF;

RA Hilaire E., Young S.A., Willard L.H., McGee J.D., Sweat T.A.,

RA Chittoor J.M., Gulkema J.A., Leach J.E.;

"Induction of peroxidase gene POC1 during the incompatible interaction

RT of rice with Xanthomonas oryzae pv. oryzae.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

REL; AF247700; AAF65464.2; -.

RESE; P22195; ISCH.

RINTS; PRO0141; peroxidase.

Pfam; PF00141; peroxidase; 1.

PROSITE: PS00458; PEROXIDASE.

PROSITE: PS00435; PEROXIDASE.

PROSITE: PS00436; PEROXIDASE_2; 1.

PROSITE: PS00436; PEROXIDASE_2; 1.

PROSITE: PS00436; PEROXIDASE_2; 1.
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Ehrhartoideae; Oryzeae; Oryza
MCBI_TaxID=4530;
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NLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIR
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                                                                                                        TALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFD
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01-JAN-1998;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
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PROSITÉ; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; PEROXIDASE.
SEQUENCE 315 AA; 33558 MW; B6F
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EMBL: X91172; CAA62597.1; -.
HSSP: P22195; ISCH.
InterPro; IPR002016; Peroxidase.
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STRAIN-CV. HANDSOME HALL;
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Pred. No. 1.
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Best Local
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01-NOV-1996 (TIEMBLICEL 01, Last sequence update)
01-DEC-2001 (TIEMBLICEL 19, Last annotation update)
Cationic peroxidase.
Stylosanthes humilis (Townsville stylo).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot9; Reurosids I; Fabales; Fabaceae; Papilionoldeae; Aeschynomeneae; Stylosanthes.
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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SEQUENCE
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PROSITE; PS00435; PEROXIDASE_2; 1.

PROSITE; PS00436; PEROXIDASE_2; 1.
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Reimmann C., Ringli C.,
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                                              STRAIN-PATERSON; TISSUE-LEAF
                                                                     SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=35628;
                                                                                                                                                                                                                                                                                                                                                                                        Q41324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGD:GNLAPIDVQT 235
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317 AA;
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25 POTENTIAL.
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317 P
; 32875 MW;
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; CEC727D0DA30E311 CRC64;
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Pred. No. 5e-67;
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                                                                                                                                                                                                                                                                                 01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
Interpro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curtis M.D., Nourse J.P., Manners J.M.;
"Nucleotide sequence of a cationic peroxidase gene forage legume Stylosanthes humilis.";
Plant Physiol. 108:1303-1304(1995).
EMBL; L37790; AAB02554.1;
HSSP; P22195; 18CH.
                                                                                      Chittoor J.M., Leach J.E., White F.F.;
"Differential induction of a peroxidase gene fof rice by Xanthomonas orygae pv. orygae.";
Mol. Plant Microbe Interact. 10:861-871(1997).
                                                                                                                                                                                                                                                                                                                                      022441
                                                               EMBL; AF014470; AAC49821.1;
HSSP; P22195; 1SCH.
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             POXGX9
                                                                                                                                                                                                                                                                                                                      022441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002016; Peroxidase
                                                                                                                                          MEDLINE=97449844; PubMed=9304860;
                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                      Peroxidase.
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es 182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHDCFVQGCDASVLLDDTSTFTGEKTAFPNVNSARGFDVIDTIKSQVESLCPGVVSCADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTLMQCLVAVSLLSC-VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLF
                                                                                                                                                                                                                                                                                                                                                                                                   TGTSGQIRTNCRKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LALAARDSVVALGGPSWNVQLGRRDSTTASLNSANSDLPGPSFNLSGLISAFSKKGFTAK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PISKVCFIIFMCLNIGLGSGQLSSNFYATKCPNALSTIKSAVNSAVSKEARLGASLLRLH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDTAYFTNLLSRRGLFHSDQELFN-GGSQDALVRQYSASASLFNADFVAAMIRMGNVGVL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELVTLSGAHT IGQARCTTFRTR I YNESNIDPSYAKSLQGNCPSVGGDSNLSPFDVTTPNK
                                                                                                                                                                                                                                                                                 (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AA;
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                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33844 MW;
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57.8%;
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Last sequence update)
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Pred. No. 1.1e-66;
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01-JAN-1998
01-DEC-2001
                                                                                                                                             Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
SEQUENCE 317 AA; 32863 MW;
                                                                                                                                                                                                                    STRAIN-IRBB10; TISSUE-LEAF;
MEDLINE-97449844; PubMed-9304860;
Chittoor J.M., Leach J.E., White F.F.;
Chittoor J.M., Leach J.E., White F.F.;
Differential induction of a peroxidase gene family during infection of rice by Xanthomonas oryzae pv. oryzae.";
Mol. Plant Microbe Interact. 10:861-871(1997).
EMBL; AF014467; AAC49818.1;
HSSP; P22195; 18CH.
                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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TAGQIRRNCRVVN 312
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                          LLRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCAD 117
                                                MASATNSSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGAS
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Pred. No. 2.7e-66;
4; Mismatches 83;
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Pred. No. 1.
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US10047825/runat_26042003_111958_7132/app_query.fasta_1.455
-DB-Genbmbl -OFMT-fastap -SUFFIX=rge -MINMANCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM-ext -HEAPSIZE=500 -MILLEN=0 -MAXIEN=200000000
-USER=US10047825_eCGN_1_1_1687_@runat_26042003_111958_7132 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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36: em_htg_mam:*
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39: em_htg_o_mus:*
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41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length DB

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Description

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ALIGNMENTS

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buffel grass
Thesis (1994) Botany,
Thesis (1994) Botany,
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[ bases 1 to 1335)
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/cultivar="Biloela"
/db_xref="taxon:35872"
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/db_xref="GI:520568"
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/clone_lib="lambda gt
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t. Lucia, Brisbane, Queensland,
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Rosidae; eurosids II; Malvales; Malvaceae; Gossypium
(PGR99-129)
Plant Physi
                       1 (bases 1 to 1369)
Assighetse, K., Cuny, G., Valette, C., Delannoy, E., Bro Jalloul, A., Daniel, J.-F., Geiger, J.-P. and Nicole, M. Cloning and Characterization of a Bacterial-Induced
                                                                                                                Gossypium hirsutum bacterial-induced AF155124 AF155124.1 GI:5453378
               Peroxidase-Encoding
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Assigbetse,K., Cuny,G.,
Jalloul,A., Bresson,E.,
Direct Submission
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DTIKUNVEAACSATVSCADILALAARDGVALLGGETWQVPLGRSDARTASQSAANNQI
PSPFANLATLTSSFAAKGLSTRDLTALSGGHTIGLARCTFRGRIYNDTNIDANFAAT
RRANCPASGGDNNLAPLDIQTFTREDNDYFRNLVARRGLLHSDQELFNGGSQDALVRT
YSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCRVVN"
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735. .737
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/cultivar="Reba B50"
/db_xref="taxon:3635"
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/evidence=not_experimental
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/note="disulfide bond"
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/db_xref="GI:5453379"
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                                     Oryza sativa (japonica cultivar-group) (cultivar:Nipponbar clone:OSJNBa0082C09.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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             Sasaki,T.,
Matsumoto, T. and Katayose, Y. va nipponbare (GA3) genomic DN
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a valiable and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
ThrTrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsn 153
                      TGTTCGAATTGATTCCATAGATTCTGACGGCGACGCGCGTACGTGCAGCTCGGCGGCCA
                                                                           GACCAGATCAAGCGCAACGTCGAGCTCCTCTGCCCCGGCGTCGTCTCCTGCGCCGACATC
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Sasaki.T., Matsumoto,T. and Katayose,Y.
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Submitted (25-Apr-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (P-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between then are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DN
clone: P0599C12
Published Only in Database (2001)
2 (bases 1 to 135792)
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Location/Qualifiers
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                            NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                             Submitted (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakidenias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
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Sasaki, T., Matsumoto, T. and Yamamc Direct Submission
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OSJNBA0016D02, *** SEQUENCING IN PROGRESS
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ACGTTCACCGGCGAAGAGAGAGCGCCGCCCGAACGCCAACTCGGCCCCGGGTTCGAGGTG
                                                                                                                                                                                                                                                                                                                                                      GTTGTCTGGTGGGGTTGGTTGCAGGGATGTGACGGCTCGATCCTGCTTGACGACACGTCG 76726
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                                                                                                                  ------LeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThr 145
                                                                                                                                                    TGACACGTACGTGAAACCACCCGTACGTCACTGAAATTTTACCAGTGGCTGACATGTTCT 76966
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                                                 ACGGCGAGCCAGAGCGCGAACAGCAACCTGCCGGGGCCCGGGTCGAGCCTCGCCACG
                                                                                                                                                                                                    ATCCTCGCCCTCGCCGCCGCGACGGCGTCAACCTGGTCAGTGTACTACATACGCTGCTC 76906
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cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="05JNBa0016D02"
/ 35607 c 35786 g 42641 t 239 others
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gene	AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE	RESULT 6 SOPRIR6 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 286 A Db 77447 T Qy 306 A Db 77507 C	Qy 246 A Db 77327 A Qy 266 G Db 77387 C	Qy 186 A Db 77147 G Qy 206 A Db 77207 A Qy 226 G Db 77267 G
/organism="Spinacia oleracea" /organism="Spinacia oleracea" /orb_xref="taxon:3562" /clone="pc23" /tissue_type="leaves" /tissue_type="leaves" /tissue_type="stems" /tissue_type="stems" /tissue_type="otyledons" /clone_lib="lambda UNIZAP-XR/SOC1" /dev_stage="four-weeks-old plants grown in short days" /gene="prxr6" /1. 930 /gene="prxr6" /EC_number="111.1.7" /codon_start=1 /evidence=experimental /product="peroxidase" /protein_id="CAA71493.1" /db_xref="GI:1781332"	Simon, P. Diveristy and conservation of plant peroxidases Plant Peroxidase Newsletter 1, 4-7 (1993) (bases 1 to 1091) Simon, P. Direct Submission Submitted (10-JAN-1997) P. Simon, University of Geneva, Lab. Plant Blochemistry and Physiology, Uni-Bastions, Place de Luniversite 3, CH-1211 Geneva 4, SWITZERLAND LOCATION/Qualifiers 1. 1091	SOPRXR6 1091 bp mRNA linear PLN 15-JAN-1997 Y10467 Y10467 Y10467 Y10467 101:1781331 peroxidase; prxx6 gene. Spinacia oleracea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia. 1 (bases 1 to 1091)	AlaAlaMetIleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArg 305 ::: ::::: ::: TCCGCCATGCTCAAGATGGGCAACCTGCTGCCGCTCCTCCGGCACCGCCACGGAGGTCAGG 77506 ArgAsnCysArgValValAsn 312	ASDLEULEUSETATGATGGLYLEUPheH1sSETASPGLNGLULEUPheAshGLYGLYSET 265	AlaHisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThr 205

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                      GlyAspGlyAsnLeuAlaProIleAspValGlnThrProValArgPheAspThrAlaTyr
                                                                                                                                                             AspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGly-----
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/translation="IILAYLACLSNAOLSSKHYASSCENLEKIVRKTMKQAVQKEQRM/translation="IILAYLACLSNAOLSSKHYASSCENLEKIVRKTMKQAVQKEQRMGASILRLFFHDCFVNGCDASLLLDFSTFTGEKTAISNRNNSVRGFEVIDSIKTNVEAGASIKILRLFHDLFHDCFVNGCPLSNSCKATVSCADILALAARDGVFLLGGPSMKVPLGRRDARTASLTAATNNLPAASSSLSNSCKATVSCADILALAARDGVFLLGGPSMKVPLGRRDARTASLTAATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFKDMTALSGAHTIGLARCVSFRHHIYNDTDIDANFEATRKVNCPLSNITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENNKGLSFRHITTENN
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Linum usitatissimum peroxidase FLXPER4 (PER4) mKNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omann, F. and Tyson, H. Direct Submission
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Linaceae; Linum.
1 (bases 1 to 1176)
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Conservative:
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Gaps:
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2 (bases 1 to 1238)

Yamada, K., Banh, J., Chang, C.H., Chang, E., Dale, J.M.,

Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.I., Tang, C.C.,

Gorlumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kin, C., Lam, B.,

Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.,

Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,

Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               to this work. Shinozaki, K. (RIKEN /PGEC) contributed equally to this Location/Qualifiers.
                                                                                                                                                                                                                                                 /gene="At5g05340"
57, .1021
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1238)

Yamada, K., Liu, S., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karilin-Neumann, G., Kawai, J., Kim, C., Lam, B., Jin, J., Miranda, M., Narusaka, M., Ngyen, M., Palm, C.J., Sakurai, T., Toriumi, M., Sakurai, T., Marusaka, M., Ngyen, M., Palm, C.J., Sakurai, T., Saku Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., S Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Arabidopsis Full Length cDNA Clones Unpublished 2 (bases 1 to 1238) Lam, B.,

Direct Submission

Submitted (03-DEC-2001) Plant Gene Expression Center, 800 Buc Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out to collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishi Satou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K. 800 Buchanan Ishida, J., the

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Conodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinan,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally GSC) and The work as PIs. Theologis, A.

pBluescript vector

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/sub_species="Nobel"
/db_xref="taxon:3562"
/clone="PC44"
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11 ValAlaValSerLeuLeuSerCysValAlaHisAlaGlnLeuSerProThrPheTyrAla
Submitted (20-MAY-1999) Hiroyuki Ito, Hokkaido University, Department of Applied Bioscience, Graduate School of Agriculture; Kita-9, Nishi-9, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail:otihechem.agr.hokudai.ac.jp, Tel:81-11-706-2500, Fax:81-11-706-3635)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiraga,S., Ito,H., Matsui,H., Honma,M. and Ohashi,Y. cDNA sequences for two novel tobacco peroxidase isoenzymes (Accession Nos. AB027752 and AB027753). (PGR99-109) Plant Physiol. 120, 1205 (1999) 2 (bases 1 to 1356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum (cultivar:Samsun clone_lib:lambda gt10 clone:tpoxC1
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
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/protein_id-"BAA82306.1"
/db_xref="Gi:5381253"
/translation-"MASLKINAIVLFILVSLLIGSSSAQLSTGFYSKSCPKLYQTVKS
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                                           Shoyama, r.

Identification and molecular characterization with structural protein-like properties

J. Biol. Chem. 274 (37), 26192-26198 (1999)
                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Scutellaria.
                                                                                                                                         peroxidase 3.
Scutellaria baicalensis cDNA to mRNA.
Scutellaria baicalensis
                                          J. Biol. Chem. 99403061
                                                                                          Morimoto,
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AB024439
  Submitted (01-MAR-1999)
            Direct Submission
                                                                                                                                                                                                       AB024439
                      Morimoto,S.
                                                                                                      (sites)
                              (bases 1 to 957)
                                                                                         S., Tateishi, N.,
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  Satoshi
                                                                                         Inuyama, M.,
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 Morimoto,
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                                                                                        Taura, F.,
  Kyushu
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                                                          AlaHisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThr
                                                                                                                                      LeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGly
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                                                                                                                  CTCATCACTTCTTTCTCTAACAAAGGCTTCACTGCCAGAGAAATGGTTGCTCTTTCTGGA
                                                                                                                                                                                           ACAGCTAGTCTGAATGCAGCCAACACCCAAATCCCAGGACCTGGACTCAATCTCAATGCC
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QIGPGGLNLNALITSESNKGFTAREMVALSGSHTIGQARCTTFHGRIXNDTNINGAFA
TGLRANCPRSGGDNNLAPLDNVSPARENNDYYRNLIGLRGLLHSDQELFNNGTADAQV
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252 c 245 g 223 t
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/protein_id="BAA77389.1"
/db_xref="GI:4760704"
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/db_xref="taxon:65409"
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                ThrPheTyrAlaSerSerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGln
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1 (bases 1 to 1144)

1 (bases 1 to 1144)
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Differential expression of peroxidase isogenes during stages of infection of the tropical forage legume Sty
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Mol. Plant Microbe Interact. 8 (3), 398-406 (1995)
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/db_xref="taxon:35628"
/clone="Shpx6"
                                                                                                                                                                                                                                                                                              /tissue_type="stem"
                                                                                                                                                                                                                                                                                                                                                    organism="Stylosanthes"
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VERSION
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 1330)
1 (bases 1 to 1330)
Hilaire, E., Young, S.A., Willard, L.H., McGee, J.D., Sweat, T.A., Chittoor, J.M., Guikema, J.A. and Leach, J.E.
Induction of peroxidase gene POC1 during the incompatible
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Oryza sativa
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                                                           CTGCACTTCCATGACTGTTTTGTCCAAGGTTGCGACGCGTCTGTTCTGTTG----TCGGGA
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LeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGly
                                        ATCAAGGCGCAGATAGAGGCCGTGTGCAATCAGACCGTCTCATGCGCCGACATCCTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-JUL-2000) Plant Pathology, Kansas State University, Throckmorton Plant Sciences Center, Manhattan, KS 66506, USA Sequence update by submitter On Jul 3, 2000 this sequence version replaced gi:7638414.
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RTSGDMNLAPLDTTTANAFDNAYYTNLLSNKGLLHSDQVLFNNGSTDNTVRNFASNAA
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aavnseprmgasllrlhfhdcfvqgcdasvllsgneqdappnkdslrgygvidsikaq
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/protein_id="AAF65464.2"
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/note="isolated after 12 hours following infiltration
incompatible strain of Xanthomonas oryzae pv. oryzae"
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O.sativa
                                                                                                                                                                                                                                                                                                                                           Oryza sativa
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                                                                                                                                                                    Reimmann,C., Ringli,C. and Dudler,R. Complementary DNA cloning and sequencing
                                                                                                                                                                                                                             Submitted (07-JUN-1992) University of Zuerich, 2
                                                                                                                                                                                                                                                          Direct Submission
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaae; Oryza.
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Oryza sativa.
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              22. .975
/EC_number="1.11.1.7"
                                                                                    /organism="Oryza sativa"
/cultivar="Nohrin"
                                                                                                             Location/Qualifiers
/codon_start=1
                                         /clone_lib="lambda ZAP
                                                         /clone="pPIR3"
                                                                       /db_xref="taxon:4530"
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                ThrCysProArg-----SerGlyGlyAspGlyAsnLeuAlaProIleAspValGlnThr 235
AACTGCCCACGGCCGACGGCAGCGGCGACAGCAACCTGGCGCCCGTGGACACGACGACG
                                                                                                       ACCGACATGGTTGCTCTCTCAGGAGCACACACGATCGGGCAGGCGCAGTGCCAGAATTTC
                                                                                                                     ProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerPro
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/EC_number="1.11.1.7"
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1 (bases 1 to 1116)
Buffard,D., Breda,C., van Huystee,R.B., Asemota,O., Pierre,M.,
Ha,D.B. and Esnault,R.
Molecular cloning of complementary DNAs encoding two cationic peroxidases from cultivated peanut cells
Proc. Natl Acad. Sci. U.S.A. 87 (22), 8874-8878 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-AUG-1990) Robert Esnault, Institut des Sciences Vegetales, CNRS, 91198 Gif Sur Yvette, France On Aug 15, 1996 this sequence version replaced gi:166472.
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YSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNCRKTN"
1 214 c 213 g 340 t
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NSAVAKEARWGASLIkihehdcfyQgcdasyllddtsnfygktagphanstikgebyi
DTIKSQVESLLPGYVScadilavaardsyvaldgaswhyllgredsttaklssanst
PAPFFNLSGLISAFSNKGFTTKELYTLSGAHTIGQAQCTAFRTRIYNESNIDDTYAKS
                                                                                                                                                                                                                                                                                                                                  /gene="PNC1"
13. .963
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/product="cationic peroxidase"
/protein_id="AAB06183.1"
/db_xref="GI:1491776"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Arachis hypogaea"
/db_xref-"taxon:3818"
/clone="prxPNC1"
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                                                              282 AlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyValLeuThrGlyThrAla 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 TCTAATTTTTATGCCACAAAATGTCCCCAATGCACTTTCAACAATTAAGTCAGCAGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LeuMetGlnCysLeuValAlaValSerLeuLeuSerCysValAlaHisAlaGlnLeuSer 25 ::: |||||||||||||
GlyGlnIleArgArgAsnCysArgValValAsn 312
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|GGCCAAATTAGAACCAATTGCAGGAAGACCAAC 960
                                                                                                                                                                                                                                                                                                      SerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThr 181
:::||| ::: ::::::::
AATCTTAGTGGCCTTATCTCTGCTTTCTCCAACAAAGGTTTCACAACAAAAGAACTCGTT 567
                                                                                                 AsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsn
                                                                                                                                                                                                                             TyrGlyAspThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArg
                                          AATGGTGTATCCACTGATTCCCAAGTCACTGCTTATAGCAACAATGCTGCAACTTTCAAC
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SUMMARIES

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-Q-/Ggn2_1/USPTO_Spool/US10047825/runat_26042003_111957_7124/app_query.fasta_1.455
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -QUITMT=pto -NORM-ext -Pct-RSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10047825_@CGN_1_1_200_@runat_26042003_111957_7124 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NBG_SCORES=0 -WANIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDEXT=0.5 -FGAPDP=6 -FGAPEXT=7
-YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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RESULT 1
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                                                                     Oryza sativa; modification;
                                                                                                      Oryza sativa peroxidase s4235 encoding cDNA SEQ ID NO:13.
                                                                                                                                                                             AAH44077 standard; cDNA; 1156
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                                                                                                                              (first entry)
                                                                 rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea; ss.
           Location/Qualifiers 75..1058
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AAC42729
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AAC47823
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AAA68192
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Synthetic Nicotian
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Pinus radiata pero
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日
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 152-155; 258pp; Japanese.
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Hiraga S;
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in rice under varying conditions
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DB; AAB99738.
                                                                                                   ProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLysArgAsnValGlu
                                                                  CysAspGlySerIleLeuLeuAsp-----
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CCGAACGCCAACTCGGTGCGCGGGTACGAGGTCATCGACGCCATCAAGGCGCAGCTCGAG
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RESULT 2
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                                                                                                                                                                 plant; lignin; lignin biosynthetic pathway;
pinus radiata; Monterey pine; ds.
                                                                                                                                                                                                                  24-OCT-2000
        Bloksberg LN,
                                                        09-OCT-1998;
14-JUL-1999;
                                                                                      06-OCT-1999;
                                                                                                                                                Pinus radiata.
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                                                                                                                                                                                                                                                                                                                                                                          GGCAATGGCACCACGGACGCGTTCGTGCGCGCGTACGCCGACGACGACGACGTTCGCG
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                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                               peroxidase nucleotide sequence SEQ ID NO:363
         Havukkala IJ;
                                                        98US-0169789.
99US-0143811.
                                                                                      99WO-NZ00168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CCR), phenylalanine ammonia-lysse (PAL), 4-commanded (ACL), coniferol glucosyl transferase (CGT), coniferon beta-glucosidase (CBG), laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase, commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin content, composition and structure. They can be used for designing probe and primers useful for detecting similar DNA and RNA sequences in any correct and for producing a plant having altered lignin content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1224
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Hiraga S;
New set of rice peroxidase in rice under varying condidesired characteristics -
                                                                                                                                                   08-DEC-2000;
                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                                                                                                                                                                                                          Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                         AAH44080 standard;
                                           P-PSDB;
                                                                                                        (NORQ ) JAPAN MIN AGRIC FORESTRY &
                                                                                                                               10-DEC-1999;
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                                                                                                                                                                                                                                                                                          rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea; ss.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed detecting the label signal to show which genes in the set are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCys 71
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ThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThrAspIle
                                                     SerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHis 187
                                                                                                                                                                                                                                                                                                           AsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLysArgAsnValGluAla 107
                                                                                                                                                                                                                                                                                                                                                         GACGCATCGCTGCTGCACGACGACACGCCGAGCTTCACCGGCGAGAAGACGGCGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                       AspGlySerIleLeuLeuAsp.-----AlaGlyGlyGluLysThrAlaGlyPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAlaSerGlu
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                                                                                                                              SerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeuIle 167
                                                                                                                                                                                                                                                                                          AACAACGGCTCCGTCAGAGGGTTTGAGGTGATCGACGCCATCAAGTCGGCGGTGGAGACC
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                        The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coummarate:COA ligase (4CL) coniferol glucosyl transferase (CCF), coniferin beta-glucosidase (CBG) laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                          Claim 1; Page 189-190;
                                                                                                                                                                                                                                                                                                 structure
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                                                                                                                                                                       GTTGCACTTTCTGGCGGTCATACCATCGGGCAGGCGCAATGCAAGAATTTCAGAGCCCAT
                                                                                                                                                                                             ThrAlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArg
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                                                                                   ATTTACAACGAGACCAACATAGACAGTGCGTACGCCACTTCATTGCGTTCAAAGTGTCCG
                                                                                                                         IleTyrGlyAspThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysPro
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Matches:
Conservative:
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This cDNA sequence includes a coding region for the 320-amino acid shpx6 peroxidase (see AAW38217) of Stylosanthes humilis. A claimed method of engineering a plant to fungal resistance comprises introducing into cells of the plant a DNA construct comprising a promoter that is constitutively operative in the plant cell (preferably the cauliflower mosaic virus 35s promoter) and the shpx6 sequence, or a hybridising sequence or fragment that encodes an enzyme with peroxidase activity. Also claimed are plant cells harboring the DNA construct, a plant comprising such cells, and material from such a plant, especially seed, pollen, a stem segment

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                                                                                                          Plant cell transformed with Stylosanthes humilis Shpx6 peroxidase useful to confer on plants resistance to fungi, e.g. Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerctorium
                                                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                        Stylosanthes humilis Shpx6 peroxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT95782;
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                                                                                                                                                                       Goulter KC,
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                                                                                          Claim 3; Page 14-15;
                                                                                                                                              WPI; 1997-549739/50
P-PSDB; AAW38217.
                                                                                                                                                                                                                                 29-APR-1997;
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                                                                                                                                                                                       (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or a cutting. Resistance to fungi, especially Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerotorium, be conferred on cereal, legume, oilseed, sugar or fibre plants, particularly maize, banana, peanut, field pea, sunflower, tomato canola, tobacco, wheat, barley, oat, potato, soybean, cotton,
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PheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSerLeuPhe
                                           ATGGTTACTATAAGAACTTGCTAGTGAAAAAGGGTCTCTTCCACTCTGATCAACAACTC
                                                       ThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAspGlnGluLeu
                                                                                                   ACAGGCAATGGTGACAACAACTTGGCCCCAATTGACAACAACTAGTCCAACAAGGTTTGAC
                                                                                                                   -----GlyGlyAspGlyAsnLeuAlaProIleAspValGlnThrProValArgPheAsp
                                                                                                                                                              ACTGAGAGCAACATAGATCCCAATTTTGCCAAATCATTGCAAGGAAATTGCCCTAATACC
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|AAACAGCACGTCCTAATGCTAATTCAATTAGAGGTTTTGAAGTCATAGACACCATAAAA
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RESULT 6
AAH44085
                  The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed. CC in the sample plant; and (4) DNA microarrays for peroxidase gene capression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificaties of CC peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
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Вp Qy

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LeuMetGlnCysLeuValAlaValSerLeu---LeuSerCysValAlaHisAlaGlnLeu

US-10-047-825-4 (1-313)

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RESULT 8
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  Plant; lignin;
Pinus radiata;
                                                                  24-OCT-2000
                                      Eucalyptus grandis peroxidase nucleotide sequence SEQ ID NO:352.
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lignin biosynthetic pathway; Eucalyptus Monterey pine; ds.
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The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4 -hydroxylase (C4H), CC coumarate 3 -hydroxylase (C3H), phenolase (PNL), 0-methyl transferase CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (ACL), CC coniferol glucosyl transferase (CCT), coniferon beta-glucosidase (CBC), CC caffeic acid methyl transferase, caffeoyl COA methyl transferase, CCCT), coniferol oxidase, flavanol CC coumerate COA ligase, cytochrome P450 LXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, CC composition and the structure of a plant, especially eucalyptus and pine CC composition and the structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC ontent, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DNA and RNA sequences in any CC organism and for PCR amplification. The lignin content can be efficiently CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to CAAB16449 represent polynucleotide and protein sequences used in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 184; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure
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(FLET-) FLETCHER CHALLENGE FORE
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Sequence 1391 BP; 399 A; 321 ç; 307 G; 364 7 0 other;

Percent Similarity:
Best Local Similarity:
Query Match: US-10-047-825-4 (1-313) x AAA68176 (1-1391) Score: Pred. No.: Alignment Scores: 4.09e-68 899.50 71.52% 56.96% 56.08% Conservative: Mismatches: Indels: Gaps: Length: Matches: 1391 180 46 85 5

δõ B QY 246 1 MetAlaSerProThrLeuMetGlnCysLeuValAlaValSerLeuLeuSerCysValAla ATGGTCGGCTTTTCCGTCGTCGTTGTCCTTCCTTGCCACTTCGGTTATCACC---ACTGCC 302

밁 CGTTGTAAGCTCTCACCGAGTCATTATCAATCAACATGTCCGAAAGCATTGTCGATTGTT 362

Qy 멍 363 41 ArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGlyAlaSerLeuLeuArg CGAGCTGGAGTAGCAAAAGCAATCAAGAATGAGACCCGGACGGGCGCGTCCTTGCTTCGG 422 60

61 LeuPhePheHisAspCysPheValGlnGlyCysAspGlySerIleLeuLeuAspAlaGly 80

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                                 24-NOV-2000;
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            24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the cDNA sequence of a peroxidase P7X gene. The P7X gene is isolated from maize inbred line Mp307. Peroxidases reduce hydrogen peroxide or molecular coxygen in the presence of an electron donor. Plant peroxidases are involved in pathogen defence responses. DNA constructs or transcription casse comprising peroxidase P7X gene and its promoter are useful for providing nematode resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1379 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel gene encoding peroxidase P7X protein, and its for producing transgenic plants that are resistant infections .
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                                                                  AlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGly 171
                                                                                                                                                                                                                 ValArgGlyPheGluValIleAspThrIleLysArgAsnValGluAlaAlaCysProGly
                                                                                                                                                                                                                                                            SerIleLeuLeu---AspAlaGlyGlyGluLysThrAlaGlyProAsnLeuAsn---Ser
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AlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThrAspIleAsnAlaSerPhe
                      AAGAAGAATCTCAACCCAACCGACATGGTTGCACTCTCAGGAGCTCACACGATCGGACAG
                                           ArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHisThrIleGlyGln 191
                                                                                                                                                          ATCGTCTCCTGCGCCGACATCCTCGCCGTGGCCGCCAGGGACGGAGTCGTATCGCTCGGC
                                                                                                                                                                                                                                                TCCCTTCTGCTGAACGACACGTCAGGGGAGCAGAGCCAGGGCCCGAATCTAACTCTGAAC
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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set of given in AAH44071 to AAH44091. Also described are: (1) promoters for
                                                                                                                        New set of rice peroxidase genes in rice under varying conditions desired characteristics -
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P-PSDB; AAB99744.
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                    GGCGGCGACACCAACCTGGCGCCGCTGGAC - - TCCACCCCCAACGCCTTCGACAACGCC
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                   LeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAla
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(first entry) (first entry) thaliana DNA fragment SEQ ID NO: 14488. thickication: signal transduction pathway; thray; permit mapping; gene expression control; tkinay; permit transduction pathway; thaliana. 2000EP-0301439. 99US-0121825. 99US-0121825. 99US-0121826. 99US-0121826. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-0122788. 99US-012487. 99US-012487	t SEQ ID NO: 14488. PR PR PR PR PR PR PR PR PR PR PR PR PR	th SEQ ID NO: 14488. ping; gene expression control; ransduction pathway; mination sequence; ss.	PR 10-JUN-1999; PR 10-JUN-1999; PR 10-JUN-1999; PR 16-JUN-1999; PR 16-JUN-1999; PR 17-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999;	PR 06-MAY-1999; PR 06-MAY-1999; PR 17-MAY-1999; PR 11-MAY-1999; PR 14-MAY-1999; PR 14-MAY-1999; PR 14-MAY-1999; PR 14-MAY-1999; PR 14-MAY-1999; PR 18-MAY-1999; PR 19-MAY-1999; PR 20-MAY-1999; PR 20-MAY-1999; PR 21-MAY-1999;	05-MAR-199 09-MAR-199 23-MAR-199 25-MAR-199 25-MAR-199 29-MAR-199 01-APR-199		RESULT 12 AAC36625 Start XX AC36625; XX AC36625; XX
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Conservative:
Mismatches:
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The present invention describes isolated polynucleotides and proteins commarate 3-hydroxylase (C3H), phenolase (PNL), 0-methyl transferase (C(OMT), cinnamyl alcohol dehydrogenase (PNL), 0-methyl transferase (CC(OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC laccase, peroxidase, ferulate-5-hydroxylase (FSH), alpha-amylase, CC coumerate COA ligase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC content of the structure of a plant, especially eucalyptus and pine composition and the structure of a plant, especially eucalyptus and pine content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any corganism and for PCR amplification. The lignin content can be efficiently corganism and for PCR amplification. The lignin content can be efficiently corganism and for PCR amplification. The lignin content can be efficiently corganism and for PCR amplification. The lignin content can be efficiently corganism and for PCR amplification. The lignin content can be efficiently corganism and for PCR amplification and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any corganism and for PCR amplification. The lignin content can be efficiently exampled to AAB16341 to AAB16449 represent polynucleotides. AAB67908 to AAB68201 and AAB16341 to AAB16449 represent polynucleotides and primers used in the
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                                                                                                                                                                                                                                                                                                  ThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPhe 254
                                                                                                                                                                                                                                                                                                                                  CTGAAGACAAACTGTCCGACTACAGGAAGCGACAACAACCTGTCACCATTGGATCGTGTT
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1293..1298
97US-0049752
                98WO-US11921
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53..148
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149..1051
                                                                                                                      Location/Qualifiers 53..1054
                                                                                                                                                                     gene; maize;
                                                                                                                                                                                                                                      CDNA; 1355
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                                                                                                                                                                      corn; transgenic plant; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of a maize per5 cDNA clone encoding root preferential cationic peroxidase (see AAW87893). The clone was isolated by screening maize root, stem, leaf, kernel and tassel RNA using probes (see AAV63718-19) based on tobacco peroxidase conserved domains. A probe generated from per5 cDNA was used to isolate the per5 gene (see AAV63717). Regulatory sequences of the per5 gene, including the promoter, introns and 3 untranslated region (3 UTR), arguession of recombinant gene cassettes for controlling expression of recombinant gene sh selected tissue, especially the root, of transformed plants, particularly maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 91; 150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein
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                                                TCTTTAGTCAGACTGCATTTCCATGACTGCTTTGTCAAGGGCTGCGATGCTTCGGTGCTG
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                                                                                                                                                                                                                                           LeuAspAlaGly---
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                                                                                                                                                                                                                                                                                                                                                                             CTTGGCCACCCATGGGGTGGCTTGTTCCCACAGTTCTATGACCATTCGTGCCCCAAGGCG
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                                                                                                                                                            SerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCysAspGlySerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTCCATGGGTTGTCTCGTCTTGCTCTGCCTTGTTTCTTCTCCCTTCCCAGTGCCGTC
AACAATGACATCCCAGCCCCCAACAACACCTCCCCCACTATCATCACCAAGTTCAAGCGC
                        AsnSerAsnProProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArg
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Pareddy D,
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51.25%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 G; 351 T; 6 U; 0 other;
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Matches:
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Smith K,
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RESULT 15
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KW Cellu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lolium perenne; perennial ryegrass; plant; cell wall; lignification; cellulase; enzyme; lignin blosynthesis; cellulose degradation; CCOAMT; caffeoyl-CoA --O-methyltransferase; clanamyl alcohol dehydrogenase; CAI caffeic acid O-methyltransferase; OMT; cinnamate-4-hydroxylase; CAH; cinnamoyl-CoA reductase; CCR; peroxidase; PBR; ferulate-5-hydroxylase; PSH; CELL, phenylalanine ammonia lyase; PBL; 4-coumarate:COA ligase; 40 ryegrass; fescue species; molecular genetic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019
                      Novel nucleic acid encoding lignification and cellulase enzymes their related enzymes useful for modifying lignin biosynthesis a cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                      WPI; 2002-444025/47
P-PSDB; ABB78992.
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                                                                                                                                                                                                                 Spangenberg G,
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Claim 8; Fig 105; 436pp; English.

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US-10-047-825-4 (1-313) x ABN87249 (1-1295)
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Command line parameters:

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-Q-/cgn2_1/USPTO_spool/US10047825/runat_26042003_111959_7157/app_query.fasta_1.455
-DB-ISSUED_PATENTS_NA -QFMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
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                                                                                                                                                                                                                     CTCCACTCCGACCAGCAGCTCTTTAATGGAGGTTCTACAGATTCTCAGGTTACTGCGTAC
                                                                                                                                                                                                                                 PheHisSerAspGlnGluLeuPheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyr
                                                                                                                                                                                                                                                                                   GlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeu
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|GTCTTTCTACCAAGACCTTGTTGCACTCTCAGGTGCTCATACAATTGGTCAATCACGA
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US/08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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Query Match:
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US-09-615-192A-369
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LENGTH: 1171
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                                        ATTTACAACGAGACCAACATAGACAGTGCGTACGCCACTTCATTGCGTTCAAAGTGTCCG
                                                     IleTyrGlyAspThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysPro
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                                                                                      GTTGCACTTTCTGGCGGTCATACCATCGGGCAGGCGCAATGCAAGAATTTCAGAGCCCAT
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; ORGANISM: Eucalyptus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant FILE REFERENCE: 11000.1003c4U
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CTAGCTTCGTGGGCAGAAAACAGCAGCTCCGAACAACAATTCCGTGAGAGAGGGTTCGAA
                                                                                  LeuPhePheHisAspCysPheValGlnGlyCysAspGlySerIleLeuLeuAspAlaGly
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                -GlyGluLysThrAlaGlyProAsnLeuAsnSerValArgGlyPheGlu
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; TYPE: DNA
; ORGANISM: Pinus
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 Alignment Scores Pred. No.:
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                                                                                                                      SOFTWARE: F
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
                                                                                                                                                                                                                                           FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                             APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-1
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           Sequence 5, Application US/09097319A
Patent No. 6384207
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
   APPLICANT:
                                                                                                                            255 HisSerAspGlnGluLeu 260
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| 784 CACTCCGACCAGCAGCTG 801
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LENGTH: 1354 base pair
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Indianapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/097,319A
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9330 Zionsville Road
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Petolino, Joseph F.
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PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR ETLING DATE: 1997-11-21
PRIOR PELICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 361, Application US/09615192A
; Patent No. 6410718
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                                                                 ; TYPE: DNA; ORGANISM: Pinus radiata US-09-615-192A-361
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                                                                                                            SEQ ID NO 361
LENGTH: 916
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin (FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                   APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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GENERAL INFORMATION:
APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
                                     Sequence 3, Application Patent No. 6278041
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                                                                                                                                                        GAACTCTTCAACGGAGGCTCCACTGATTCGCATGTGACTAAGTACGCCTCCAACCAGAAT
                                                                                                                                                                          GluLeuPheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSer
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US-10-047-825-4 (1-313) x US-09-365-150-3 (1-975)
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; EEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sylvestris peroxidase gene
US-09-365-150-3
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CURRENT APPLICATION NUMBER: US/09/365/150
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
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ACCAACCTGGACATCAGCACCCCCAACGACTTCGACAACGACTTCACCAACCTCCAG
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                                                                                                                                       TTCGAGCAGAGACTGTTCAACTTCAACGGCAGCGGCAACCCGACCTGACCGTGGACGCC
                                                                                                                                                             PheArgGlyArgIleTyrGly------AspThrAspIleAsnAla
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                            AlaProIleAspValGlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeu 248
                                                                   ACCTTCCTGCAGACCCTCCAGGGCATCTGCCCCCAGGGCGCAACAACAACGGCAACACCTTC
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MOLECU US-08-378 Alignment Pred. No.: Score: Percent Si Best Local Query Matt DB: US-10-047 Qy 10 Db 51	H		RESULT US-08- Sequ Pate GEN A T T N C C	Oy Db	, D	Qу
ANDEDNESS: OCLOGY: lind ULE TYPE: 1 '588-23 Scores: Scores: Similarity: Similarity: Leuvalalava: Ill :: TTGGTTGCAAT:	DATE: ICATION: 800 ICATION: 800 AGENT INFORMATION: Seay, Nicholas J. ATION MUMBER: 27,386 CE,DOCKET MUMBER: 11-229- NICATION INFORMATION: NE: (608) 251-2484 : (608) 251-2484 : (608) 251-9165 FOR SEQ ID NO: 23: CHARACTERISTICS: 1270 base pairs nucleic acid	CITY: Madison STATE: WI STATE: WI COUNTRY: USA ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UNMERR: US/08/378,588	8 378-588- ence 23, nt No. 5 EFRAL INE PPLICANT ITLE OF ITLE OF UMBER OF ORRESPON ADDRESS STREET: STREET:	695 AGCATGATCAAGCTGGGCAACATCAGTCCCCTGACCGGCACCAACGGCCAGATCCGCACC 954 307 AsnCysargValValasn 312 ::: :::	67 ASPANALEUVANARGGINTYRSERANASERANASERLEUPHEASNANAAASPPHEVANANA 28	249 SerArgArgGlyLeuPheHisSerAspGlnGluLeuPheAsnGlyGlySerGln 266

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                                                         Sequence 23, Application US/08811094
Patent No. 5869720
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PE
                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Pinckney
           E: Nicholas J. Seay, Quarles & Brady First Wisconsin Plaza, One South
St.,
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; MOLECULE TYPE: US-08-811-094-23
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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APPLICATION NUMBER: 08/378,588
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
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REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELECHONOE: (608) 251-2484
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MEDIUM TYPE: Floppy disk
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LENGTH: 1270 base pair
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STATE: W
COUNTRY:
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TYPE: nucleic acid
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                                                                                                                  ProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLysArgAsnValGlu 106
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AlaSerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeu 166
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                                                                   ThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThrThr
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03-MAR-1997
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POT-US94-11121-23
; Sequence 23, Application PC/TUS9411121
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
; TITLE OF INVENTION: PRODUCING HETEROLOGOUS PF
; NUMBER OF SEQUENCES: 23
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                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
TELEPHONE: (608) 251-9166
INFORMATION FOR SED ID NO: 23:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                       ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               STREET: Pinckney St.,
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                   CLASSIFICATION:
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: PCT-US94-11121-23
                                                                                                           259 GluLeuPhe-----AsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSer
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                 AlaSerLeuPheAsnAlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyVal 296
                                                                                                                                                                                   PheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAspGln
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US-09-365-150-1
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CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 975
TYPE: DNA
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APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
TITLE OF INVENTION: NO. 6278041el Peroxidase
FILE REFERENCE: S-31081P1
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                                                                                                        AlaSerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeu 166
                                                                                                                                  GTTGCCTTGGCGAAGGTCCGTCATGGCAAGTACTTTTTGGCAGAAAAAACAGCTTAACA
                                                                                                                                                          ThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThrThr 146
                                                                                                                                                                                    AlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGly 126
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                                                                                                                                                                                                                                                                                              GGTTGTGATGGATCCATTTTATTAGACACAGATGGGACTCAAACTGAGAAAGATGCAGCT
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                           ACACCACTATTCACCAACAAGGGAATGGATTTAACTGATCTTGTTGCTCAATCAGGTGCA
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GENERAL INFORMATION:
APPLICANT: Lagrimini, Mark
APPLICANT: Lesai, Nalini
TITLE OF INVENTION: No. 6278041el Peroxidase Gel
FILE REFERENCE: S-31081pl
CURRENT APPLICATION UNMBER: US/09/365,150
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 975
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                                                  ACCGACGCCCGCCGGCGCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAAC
                                                                                                               GACAGCACCTGCCCCAACGTGACCAGCATCGTGCGCGGGGGTGATGGACCAGCGCCAGCGC
                                                                                                                                            AlaSerSerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAla 49
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                                                                              SerGluGlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGln 69
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 -GluLysThrAlaGly 86
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TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Lignin Control of Plant Current Application NUMBER: US/09/615,192A CURRENT FILLING DATE: 2000-07-12 PRIOR FILING DATE: 1997-11-21 PRIOR PRIOR DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1998-09-11 PRIOR PRIOR PRIOR DATE: 1998-10-09 PRIOR FILING DATE: 1998-10-09 PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 371 LENGTH: 1522
                                                                                                                                                                                                                                                                                                                                                                    US-09-615-192A-371
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Sequence 371, Application US/09615192A Patent No. '6410718
                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
TYPE: DNA
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Havukkala, Ilkka
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Best Local Similarity:
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US-09-615-192A-371
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                                             LeuPheAsnAlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyValLeuThr
                                                                                  ACTOTTTACACCGACACTCGAACCCGCGACATTGTGATCAATTTTGCGGTGAA/CAGAGC
                                                                                                       GluLeuPheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSer
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US-09-097-319A-1
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Patent No. 6384207
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TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,319A
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                                                                                                                                           EATURE:
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   FEATURE:
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LOCATION: 4201..4425
OTHER INFORMATION: //
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OPERATING SYSTEM: PC-DOS/MS-DOS
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VENTION: Regulatory Sequences for Transgenic Plants
EQUENCES: 59
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US-09-615-192A-365
Sequence 365, Application US/09615192A
Patent NO. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard APPLICANT: Havukkala, Ilkka TITLE OF INVENTION: Materials
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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COMMAND LINE PALAMETERS.

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-NORM-EXT-7 - YGAPOP=10 -VGAPEXT=0.5 -DELOP=6 -DELEXT=7
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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    2003, 12:58:59; search time 108 Seconds
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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US-09-938-842A-1711
US-09-938-842A-60
US-09-938-842A-1714
US-09-938-842A-1980
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  Sequence 1711, Ap
Sequence 60, Appl
Sequence 1714, Ap
Sequence 1980, Ap
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ALIGNMENTS

; GENERAL INFORMATION:

Sequence 1711, Application US/09938842A Patent No. US20020160378A1

RESULT 1 US-09-938-842A-1711

; ORGANISM: Arabidopsis thaliana US-09-938-842A-1711 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1711 LENGTH: 996 APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: 2hu, Tong
APPLICANT: 2hu, Tong
APPLICANT: 2hu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24 CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22 TYPE: DNA

Alignment Scores:

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AGAAGTGCAAGCTTGAGTCAATCGAACAACATCCCTGCACCAAACAACACATTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGGAGAGTTTTTTGAGCAATTTGCGGAATCGATCAAGATGGGAAATATCTCTCCCC
                                                                                                                                                                                CGGTGTCCAAAATCCGGTGGGGACCAGATTCTCTCGGTGCTAGACATCATCAGCGCCGCG
                                                                                                                                                                                                                            AlaGlyProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLysArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTTGTCCCTCTGTCTCTGCGACAAGAGCTATGGAGGCAAACTTTTCCCCGGGTTAT
 TTGACAGGTTCTAGTGGCGAAATCAGGAAGAATTGCAGGAAGATTAACTCT
            LeuThrGlyThrAlaGlyGlnIleArgArgAsnCysArgValValAsnSer
                                                          AlaSerLeuPheAsnAlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyVal
                                                                                        CAAGTTCTGTTCAGCAGTAACGAGAAATCGAGAGAGCTTGTGAAGAAGTATGCAGAAGAT
                                                                                                              GlnGluLeuPheAsnGlyGlySerGlnAsp---AlaLeuValArgGlnTyrSerAlaSer
                                                                                                                                   AGCTTCGACAACAGCTACTTCAAGAACTTGATAGAGAACAAGGGGTTGTTGAACTCGGAC
                                                                                                                                                 ArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAsp
                                                                                                                                                                                                     ThrCysProArgSerGlyGlyAspGlyAsnLeuAlaProIleAspValGlnThrProVal
                                                                                                                                                                                                                                                                                                                     ACCATTCTATCTAAGTTTAACCGTCAAGGACTTGATATCACTGACCTTGTCGCTCTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                            GACTCCTCTGTTCTTACCGGTGGACCAAGTTGGGTTGTTCCATTGGGAAGAAGAGATTCA
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ 1D NOS: 5379
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-60
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US-09-938-842A-60
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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LENGTH: 1017
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                                                    ACCACACTTTCAACACAATTGTCACGAGATTTAACAACCAAGGTCTCGATCTCACCGAC
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1714
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STRESS-REGULATED GENES TITLE OF INVENTION: SAME, AND METHODS OF FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                 Sequence 1980, Application Patent No. US20020160378A1
CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 .
                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                 TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                  FILE REFERENCE: SCRIP1300-3
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1980
LENGTH: 1077
TYPE: DNA
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HisSerAspGlnGluLeuPheAsn-----GlyGlySerGlnAspAlaLeuValArgGln
                                                                             CTTCAACAGCTATGTCCTCAAAACGGCAGCAATACAGGGATCACCAATCTCGATCTGAGC
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                                         ThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPhe
                                                                                           TTCAACTTCAACGGGACAGGAAACCCCGACCCGACTCTGAACTCAACACTTCTCAGCAGT
                           ACACCTGATGCGTTCGATAACAATTACTTCACGAACCTTCAGAGTAACAATGGGCTTCTC
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46.56%
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: END, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR TILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2545
LENGTH: 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
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                                                                                                                                                        SerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyPro
                             GTTTCGAACTCATCGAGGAAATCAAACATGCCTTAGAACAAGAGTGTCCTGAAACAGTT
                                                                                          SerIleValArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGlyAlaSer
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61.47%
46.79%
46.10%
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Alignment Scores: Pred. No.: Score:
                                                                     ; TYPE: DNA
; ORGANISM: Arabidopsis
US-09-938-842A-1273
                                                                                                              CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 50/300,111
PRIOR FILING DATE: 2001-66-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1273
LENGTH: 966
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1273, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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ArgValValAsnSer
                                                                       IleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCys 308
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                                                 ATCAGAATGGGAAACATTTCG-
                                                                                                              CTAGTGGAGGCTTATAGTCGGAGCCAGAGCTTGTTTTTCAGGGACTTCACATGTGCGATG
                                                                                                                                             LeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMet
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2325
LENGTH: 1059
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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AlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSer---ProArgAsp ::::||| ||| ||| |||
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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US-09-938-842A-1632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1632, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                       SEQ ID NO 1632
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPP1300-3
                                                                                                                                                                                                                                                                    TYPE: DNA
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US-10-101-736-3
                     Sequence 3, Application US/10101736
Publication No. US20030041351A1
GENERAL INFORMATION:
APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo APPLICANT: Co., Ltd.); Randy Dale Allen (Texas tech University)
TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics
TITLE OF INVENTION: for producing cotton fibers from these cotton plants
             FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/101,736
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; VOLUME: 173
; PAGES: 681-687
; DATE: 1988
US-10-101-736-3
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NUMBER OF SEQ ID NOS:
SEQ ID NO 3
LENGTH: 1062
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PUBLICATION INFORMATION:
AUTHORS: Kazuhito FUJIYAMA et al.
TITLE: Structure of the horseradish peroxidase
JOURNAL: European Journal of Biochemistry
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NAME/KEY: CDS
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TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics
TITLE OF INVENTION: for producing cotton fibers from these cotton plants
FILE REFERENCE: 204552015600
CURRENT APPLICATION NUMBER: US/09/834,659
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US/09/347,669
PRIOR APPLICATION NUMBER: US/09/347,669
RIGH APPLICATION NUMBER: US/09/347,669
RIGH FILING DATE: 1999-07-05
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 1062
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LOCATION: (1)...(1062)
PUBLICATION INFORMATION:
AUTHORS: Kazuhito FUJIYAMA et al.
TITLE: Structure of the horseradish peroxidase isozyme
JUHRNAL: European Journal of Biochemistry
VOLUME: 173
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                                         GCTTCTTTGTCTGATGCTCAACTTACCCCTACCTTCATCGACAATTCATGTCCTAATGTC
                                                                                                             TCTTCTTCTACTTTGTTCACTTGTATAACCTTAATCCCCATTGGTATGTCTTATTCTTCAT
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                                                                                      GENERAL INFORMATION:

APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo Co., Li
APPLICANT: Randy Dale Allen (Texas tech University)

APPLICANT: Randy Dale Allen (Texas tech University)

TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics

TITLE OF INVENTION: producing cotton fibers from these cotton plants
                                                                                                                                                                                  Sequence 3, Application US/09834656 Patent No. US20020049999A1
CURRENT APPLICATION NUMBER: US/09/834,656
CURRENT FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
                                                                         FILE REFERENCE:
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AUTHORS: Kazuhito FUJIYAMA et al.
TITLE: Structure of the horseradish peroxidase isozyme
JOURNAL: European Journal of Biochemistry
VOLUME: 173
PAGES: 681-687
DATE: 1988
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LOCATION: (1)...(1062)
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CCTACTCTCAACACTACTTATCTCCAAACTCTTCGTGGACTATGTCCCCTCAATGGTAAT
                                  ThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGly
                                                                       AATCAGTGTCGGTTTATTATGGACAGATTATACAACTTCAGCAACACCGGTTTACCCGAT
                                                                                                                                          GTTGGCCTCAACCGTTCTTCTGATCTCGTTGCACTGTCCGGGGGGCCCACACATTTGGTAAA
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Query Match:
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LENGTH: 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR TRICK STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES STATES S
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES
TITLE OF INVENTION: SAME, AND METHODS OF U
FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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RESULT 13
US-09-938-842A-1457
; Sequence 1457, Application US/09938842A
; Patent NO. US20020160378A1
· GENERAL INFORMATION:
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                                PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1457
LENGTH: 1062
                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
       ORGANISM: Arabidopsis thaliana
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ArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCysArg 309
                                                        ValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMetIle
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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US-09-938-842A-2559
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LENGTH: 1011
TYPE: DNA
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
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160 ThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAsp 179
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                                                                                                                                                                AlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeu 139
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                                                                                 GlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProPro 159
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US-09-938-842A-1518
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; LENGTH: 987
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1518
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                                              US-10-047-825-4 (1-313) x US-09-938-842A-1518 (1-987)
                                                                                                        Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR PILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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        CysLeuValAlaValSerLeuLeuSerCysVal--
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                                                                                                                                                                                                                                                                                                              973 TCTGCGGTTAAT 984
                                                                                               269 LeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMet 288
                                                                                                                                                                                                                               673 CCAACATTTTTGGCGCAGCTTCAAACACAATGTCCCCCAAAACGGCGAGGGTTCAGTGCGC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 AlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGlyAspGlyAsnLeu 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AsnProProProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGly 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 TrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSer 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThr 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGly 55
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                                      ArgvalvalAsn 312
                                                                       SerArgArgGlyLeuPheHisSerAspGlnGluLeuPheAsnGlyGlySerGlnAspAla 268
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Search completed: May 3, 2003, 13:53:55
Job time: 114 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US10047825/runat_26042003_112042_7654/app_query.fasta_1.455
-DB-EST -QFMT-fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MATRIX=oligo -TRANS-human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE-quality -THR_MIN=16 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10047825_@CGN_1_1_1456_@runat_26042003_112042_7654 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPPOP=60 -XGAPPEXT=60 -FGAPPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	LOCUS DEFINITION	BG842311
<pre>1 (bases 1 to 538) Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	Zea mays .	Zea mays.	EST.	BG842311.2 GI:14244343	sequence. BG842311	BG842311 538 bp mRNA linear EST 29-MAY-2001 MEST29-D08.T3 ISUM4-TN Zea mays cDNA clone MEST29-D08 3', mRNA	

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                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                           205 ThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGly 224
                                                                                                                                                                                            123 ACCAACCTGCTGTCGCGGAGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGG
                                                                                                                                                                                                                            245 ThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAspGlnGluLeuPheAsnGlyGly 264
                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                           3 ACCGACATCAACGCCTCCTTCGCGGCGCCCGCGGCAGCAGACGTGCCCGCGGTCCGGCGGC
                                                                               ValAlaAlaMetIleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIle 304
                                                                                                                                            SerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPhe
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               ArgArgAsnCysArgValValAsnSer 313
                                                                                                                             TCGCAGGACGCCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGACTTC
                                                                                                                                                                                                                                                             GACGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTC
                                                              GTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCTGGACAGATC
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G405 Agronomy, Iowa State University, Ames, IA 50011-1010,
Tel: 515-294-0975
Fax: 515-294-2299
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On May 25, 2001 this sequence version replaced gi:14208633
Contact: Patrick S. Schnable
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
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Research 6: 791-806, 1996)."
162 c 153 g 102 t
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/tissue_type="Seedling and silk"
/lab_host="DH10B"
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/cultivar="B73"
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BACKWAD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
BACKWAD: T0 column: 6
Plate: MEST3 row: D column: 6
Seq primer: tw1412 (5'-GAAGATACCCCACCCAACC-3').
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Contact: Schnable, PS
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(515)-294-0975
(515)-294-2299
(515)-294-2299
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                                                                                                                                                                                                                                                                                                                                                                                        /note-Torgan: green seedlings; vector: pAD-GAL4; Site_1: ECORI; Site_2: XhoI; ds-cDNA molecules were generated as follows: First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with kNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybrizAP lambda vector
                                                                                                                                                                                                                                                                                                                                                         (Stratagene) and excised as pAD-GAL4 phagemids." 284 c 236 g 147 t 19 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/cultivar="B73"
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/clone="MEST3-D6"
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
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/clone_lib="ISUM4-TN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHisThrIleGlyGlnA 192
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                                                                                                                                                                                                                                                            AI374530
AI374530.1
EST.
                                                                                                                                                                                                                                                                                                                                     AI374530
MEST3-D6.
                                                    Expressed Sequence Tags
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
                                                                                                Ven,T.J., Ashlock,D.A. and Schnable,P.S.

Wen,T.J., Ashlock,D.A. and Schnable,P.S.

Maize Seedlings
                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                             Zea mays.
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Agronomy, Ames, (515)-294-0975
                                   State University
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a 147 c 166 g 68 t
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                                      TITLE
   JOURNAL
                                                                                             AUTHORS
                                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 MetIleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsn 307
                                                                                                                                                                                                                                                                                                                                                                                       TGCCGGGTCGTCAACAGC 270
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                                                                                                                                                                                                                                                                            T18410
230 bp mRNA linear EST 17-OCT-1996 6c02d10t7 etiolated seedling Zea mays cDNA clone 6c02d10 5' end similar to similar to peroxidase, mRNA sequence.
                                                                   Shen, B., Carneiro, N., Torres-Jerez, I., Ste Helentjaris, T., Baysdorfer, C., Almira, E.,
                                                                                                                                                                                                                          T18410.1 GI:474233
EST.
                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceœa; PACC
                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                           2ea
                                  Partial sequencing and mapping of clones
                                                                                                                          clade; Panicoideae; Andropogoneae; Zea.
                     libraries
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Seq primer: P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
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                                                                                                             (bases 1 to 230)
                                                                                                                                                                                                       mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schnable@iastate.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        follows. First-strand cDNA was prepared from oligo-dr selected mRNA by priming with an Xhol oligo-dr primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with Xhol and size-selected. The resulting molecules were directionally cloned into the EcoRI and Xhol sites of the Hybrizap lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECCRI; Site_2: XhOI; ds-DNA molecules were generated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="%XL1-MFR Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="MEST3-D6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/cultivar="B73"
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 26,
1085-1101 (1994)
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Matches:
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                                                                                      Stevenson, R., McCreery, T.,
                                  from
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                                                                      Ferl, R.,
                                                                      Habben, J. and
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RESULT 6
BE366146
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                                                                                                                     118
                                                                                                                                                             21 HisAlaGlnLeuSerProThrPheTyrAlaSerSerCysProAsnLeuGln 37
                                                                                                                                                                                                                                  CACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAG 168
                                                                                                                                                                                                          ATGGCGTCTCCCACCTTGATGCAATGCCTGGTCGCCGTTTCCCTCCTCTCTGTGTCGCC
BE366146
369 bp mRNA linear EST 20-JUL-2000 PIL-31_A02.bl_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gainesville, FL 32611-(
ph: 904-392-1928, ext.
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interdisciplinary Center for Biotechnology Research
DNA Sequencing Core
University of Florida
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ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: helnjars@ccit.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ax: 510-727-2035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: ZipLox; Site_1: Sall; Site_2: NotI; oligo-dr selected mRNA was prepared from above ground tissue from10 day-old etiolated seedlings. ds-cDNA was prepared by priming with a NotI oligo-dr oligomer and the second strand by RNase-nicking of the DNA:RNA hybrid with DNA POLI fill-in. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and the size-selected. These were directionally cloned into the policy selected. These were directionally cloned into the size-selected. These were directionally cloned into the selected.
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82 c 60 g
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/lab_host="DH10B"
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/clone="6c02d10"
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                                                                                                                                                                                                        52 GlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCys
                                                                                                                 AspGlySerIleLeuLeuAspAlaGlyGlyGluLysThrAlaGlyProAsn 88
                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clade; Panicoideae; Andropogoneae;
1 (bases 1 to 369)
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BE366146.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An EST database from Sorghum: pathogen-induced plants
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706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-week-old sorghum plants 48 hr after inoculation;
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRW42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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REFERENCE
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BG411665
BG411665.1
                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The University of Georgia, De
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 583 0210
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                         EST
                                                                                                                                                                                          AW287460 434 bp
LG1_228_C02.b1_A002 Light Grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30502-7271, USA
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                                                                                    Sorghum bicolor
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                                                                                                     sorghum
                                                                                                                                          AW287460.2
                                                                                                                                                                           sequence
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                (bases 1 to 434)
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128 c 107 g 78 t
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/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: xhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
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Gingle, A.,

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On Jan 6, 2000 this sequence version replaced gi:6677304.
Contact: Cordonnier-Pratt MM
                                   Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                              Unpublished (2002)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                             1 (bases 1 to 476)
Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C.,
Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                 sorghum bicolor
                                                                                                                                                                                                                                                                                                                                             BM324451.1 GI:18063120 EST.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860 Fax: 706 583 0210
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Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                        pathogen
                                                                                                                                                           An EST database from Sorghum:
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/Glone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
/seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
/The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 152 c 125 g 86 t
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/db_xref="taxon:4558"
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ORIGIN

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Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or To sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 473

POLYA-NO.

Location/Qualifiers

1. 476

Source

//cpanism="Sorghum bicolor"
/clone_lib="Pathogen:infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="4"/week-old seedlings infected with
Colletotrichum graminicola"
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
Site_1: Xho; Site_2: EcoRI; Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old Fahva[1, a sorghum faminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from the bast plant, no effort was made to eliminate ESTs deriving from the pathogen."

BASE COUNT

78 a 164 c 138 g 96 t
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 265
                                              205 CAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTTGTTCAAGGTTGC
           72 AspGlySerIleLeuLeuAspAlaGlyGlyGluLysThrAlaGlyProAsn
                                                         52 GlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCys
1.94e-25
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Matches:
Conservative:
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RESULT 10 BE601026 REFERENCE ACCESSION VERSION COMMENT SOURCE KEYWORDS DEFINITION Locus TITLE JOURNAL ORGANISM An EST database from Sorghum: pathogen-induced Unpublished (2000)
Contact: Cordonnier-Pratt MM 1 (bases 1 to 479) Cordonnier-Pratt, M.-M., Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; clade; Panicoideae; Andropogoneae; Sorghum. EST BE601026 479 PI1_96_A03.b1_A002 Pathogen Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology Sorghum bicolor BE601026.1 BE601026 mRNA sequence. GI:9856099 Gingle, A., 479 induced mRNA 1 d 1 (PI1) Dean, R., linear) Sorçhum Sudman, M. and Pratt plants EST 18-AUG-2000 bicolor cDNA, Tracheophyta; aceae; PACC

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REFERENCE
AUTHORS
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LOCUS
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Best Local Similarity:
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                                                                                                                                                                                              ORGANISM
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                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 480)
                                                                                                                                                                                  sorghum.
                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                              mRNA sequence.
BE366914
                                                                                                                                                                                                                                                                                                                    PI1_42_B10.b1_A002 Pathogen induced
Contact: Cordonnier-Pratt MM
                        Unpublished (2000)
                                                                            Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt
                                                                                                                                                                                                                                                        BE366914.1 GI:9308471
                                                                                                                                                                                                                                                                                                                                             BE366914
                                   An EST database from Sorghum: pathogen-induced plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 706 542 1860 Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=Torgan: Anthracmose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracmose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the cathogon.
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Matches:
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1 (PI1) Sorghum bicolor cDNA,
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FEATURES
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Best Local Similarity:
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                                                                      Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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PI1_80_B04.b1_A002 Pathogen
mRNA_sequence.
                                                                                                                                                                                              sorghum
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 706 542 1860 Fax: 706 583 0210
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                                                                                           (bases 1 to 480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks old) exhibit juvenile susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING; While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."
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/note="Organ: Anthracnose-infected leaves from
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                                 pathogen-induced plants
                                                                      Dean, R., Sudman, M.
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RESULT 13
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Query Match:
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BE599526
BE599526.1 GI
,L.H.
An EST database from Sorghum: pathogen-induced plants unpublished (2000)
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Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                               1 (bases 1 to 487)
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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PI1_88_F01.b1_A002 Pathogen
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two-week-old sorghum plants 48 hr after inoculation:
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45.
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
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to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
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/db_xref="taxon:4558"
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d 1 (PI1) Sorghum
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bicolor cDNA,
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RESULT 14
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                                                                     REFERENCE
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                                             AUTHORS
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No.:
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
An ES
                                                    Sorghum bloolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 495)
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                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                  PI1_94_C12.b1_A002 Pathogen induced
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                                        Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                  sorghum.
                                                                                                                                                                                                                               BE600529.1 GI:9855602
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  EST database from Sorghum:
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/db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Corgan: Anthracnose-infected leaves from
/note="Corgan: Anthracnose-infected leaves from
/note="Corgan: Anthracnose infected leaves harvested 1: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 63)
Cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
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bicolor cDNA,
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BASE COUNT
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                                                                                                                                                                                                                                                                      BE594365
                                                                                                                                                                                                                                                                                            RESULT 15
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AUTHORS
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Sciences Building, Rm.
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BE594365.1
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PI1_32_E10.b2_A002 Pathogen i
                                                                                                                        sorghum
                                                                                                                                              EST
                                                                                                                                                                                                         mRNA sequence.
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poclade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 522)
                                                                                                      Sorghum bicolor
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/clone_lib="Arthogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants (BTX 623
site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of
Collectorichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
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induced 1 (PI1) Sorghum
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bicolor cDNA,
                                                                                     Tracheophyta;
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JOURNAL COMMENT
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Search completed: May Job time : 1086 secs
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                                                                                                                       72 AspGlyScrIleLeuLeuAspAlaGlyGlyGluLysThrAlaGlyProAsn 88
                                                                                                                                                                                                                     52 GlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCys
                                                                                              An EST database from Sorghum: pathogen-induced plants Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
Site_2: EcoRI; Two-week-old sorghum plants (Solate FRW42I of Collectorichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH-0.1 -LOOPELT-0 -LOOPEXT=0
-UNITS=bits -START=1 -END--1 -MARIX=blusme02 -TRANS-blusman40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTEMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER=US10047825_@CGN_1_1_1455_@runat_26042003_111958_7143 -NCPU-6 -TCPU-3
-NO_MAR_TIMEOUT=10 -THREADS=1 -XGAPOD=10 -XGAPEXI=0.5 -FGAPOXT=7
-YGAPOP=10 -YGAPEXI=0.5 -DELOP=6 -DELEXI=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 AA979912 LOCUS DEFINITION ACCESSION		444	444 310				31 32															ωΝ	
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IleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGlyAspGly
                             CACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCGGCCGCCATCTACGGCGACACCGAC
                                            HisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThrAsp
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BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
Plate: MEST3 row: D_column: 6
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(515)-294-0975
(515)-294-2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: green seedlings; Vector: pAD-GAL4; Site_1: ECORI; Site_2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
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/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/clone="MEST3-D6"
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/cultivar="B73"
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Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Contact: Cordonnier-Pratt MM
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LG1_349_F09.
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Sorghum bicolor
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                                                                                                                                                                          /db_xref="taxon:4558"
/clone_lib="ight Grown 1 (LG1)"
/clone_lip="ight Grown 1 (LG1)"
/note="organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: xhoI; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
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                 uArgGlnGlnThrCysProArg-----SerGlyGlyAspGlyAsnLeuAlaProIleAs
                                                                  CAAGAACTTCAGGGACCACATCTACAACGACACCAACATCAACCAGGGCTTCGCGAGCTC
                                                                                   sThrThrPheArgGlyArgIleTyrGlyAspThrAspIleAsnAlaSerPheAlaAlaLe
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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Sequences have been trimmed to exclude PolyA, vect
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Fax: 706 583 0210
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Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and An EST database from Sorghum: developing embryos
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EM1_47_E12.b1_A002 Embryo
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/note-"Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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AW672124
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                                                                                                                                                          Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-72
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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1 (bases 1 to 625)
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                                                                       quality sequence
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
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Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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                                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA
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Sequences have been trimmed
below Phred quality 16. The
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Si
EcoRI; The library was made from poly-A RNA in the
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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Best Local
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poc
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed to exclude
below Phred quality 16. The threshold f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYA-No.
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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BE362356
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Contact: Cordonnier-Pratt MM
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                                                                                              /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: Dark-grown seedlings; Vector lambda ZAP with seedlings of the cloning vector lambda ZAP with seedlings; Vector lambda ZAP clones to be sequenced were prepared by mass excision.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                 , L.H.
An EST database from Sorghum:
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                  EST.
                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                    clade; Panicoideae; Andropogoneae;
l (bases 1 to 615)
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Sequences have been below Phred quality
                                                                                                                          Cordonnier-Pratt, M.-M.,
                    Email: mmpratt@uga.edu
                              706 542 1860
706 583 0210
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector: Info Library w
made from poly-A RNA in the cloning vector lambda ZAP
Clones to be sequenced were prepared by mass excision
a 215 c 186 g 113 t
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/db_xref="taxon:4558"
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Submitted (25-APR-2002) Maize
Missouri, Columbia, MO 65211,
Location/Qualifiers
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Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
Overgo Probes
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/db_xref="MaizeDB:634070"
/db_xref="taxon:4577"
/clone="PC0073925"
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resc for barley genomics: Blumeria infected incompatible (Mla13) seedling leaf CDNA library
            Clemson University
                                                                                                                                                                                                                        Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; En
                                Clemson University Genomics Institute
                                                Contact: Wing RA
                                                             On Nov 17, 2000 this sequence version
                                                                                Unpublished (2001)
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Location/Qualifiers
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/db_xref="taxon:4513"
/clone="hy_CEA0006N05f"
/clone=lib="Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="TJC121"
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http://www.genome.clemson.edu/projects/barley.
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                                                                                                                                                        Submitted (25-APR-2002) Maize Mapping Project, University Missouri, Columbia, MO 65211, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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     assemblies
                                                                                       /organism="Zea mays"
/db_xref="MaizeDB:634730"
/db_xref="taxon:4577"
/note="this sequence is part of a project assemblies resulting from the application
                                       Library"
                                                  /clone="PC0084450"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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                                                                                         GlyAsnLeuAlaProIleAspValGlnThrProValArgPheAspThrAlaTyrPheThr
                                                                                                                                   CAGGGCCTCAATGTTGTTGATGTTGTCGCCCTCTCAGGTGGTCACACCATTGGTATGTCT
                                                                                                                                                                                                                                                  GlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHisThrIleGlyGlnAla
                                                                                                                                                                                                                                                                            AACAATGACATCCCAGCCCCCAACAACAACACTCCCCCACTATCATCACCAAGTTCAAGCGC
                                                                                                                                                                                                                                                                                                                                              ProThrTrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                ValSerCysAlaAspIleLeuAlaLeuAlaArgAspGlyThrAsnLeuLeuGlyGly
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             AACCTCCTGGCCGGCAAGGGCCTTCTAAGCTCTGATGAGATTCTGTTAACCAAGAGCGCT
                                                                 AACAACCTCTTCCCCTTGGACTTCATCACCCCTGCCAAGTTTGACAATTTTTACTACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Tel: 706 542 1860 Fax: 706 583 0210 Email: mmrrr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
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1 (bases 1 to 589)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                  /Clone_lib="Pathogen induced 1 (PII)"
/Clone_Torgan: Authracnose-infected leaves from
/note="Torgan: Authracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (Isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibilty
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
                                                                                                                                                  a
                                                                                                                                              the pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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2.31e-73
809.00
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Conservative: Mismatches:

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                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                clade; Panicoideae; Andropogoneae;
1 (bases 1 to 561)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                             BE361738
DG1_82_H08.b1_A002
                               Seq
                                               Email: mmpratt@uga.edu
Sequences have been tr
below Phred quality 16
                                                                                                                              Contact: Cordonnier-Pratt MM
                                                                                                                                     An EST database from Sorghum: dark-grown seedlings Unpublished (2000)
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BE361738
          High quality sequence stop: POLYA=No.
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Cordonnier-Pratt, M.-M., L.H.
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US-10-047-825-4 (1-313) x BE361738 (1-561)
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Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poales; Andropogoneae; Sorghum.

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/db_xref="taxon:458"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector: Instance in the cloning vector lambda ZAPy made from poly-A RNA in the cloning vector lambda ZAPy clones to be sequenced were prepared by mass excision.

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Query Match: Š 밁 Ş 밁 Ş 망 . 2 밁 Qy д Q 밁 Q В Š 밁 δÃ 밁 US-10-047-825-4 (1-313) x BE358471 (1-570) DB Pred. No.: Alignment Scores: BASE COUNT ORIGIN FEATURES COMMENT TITLE JOURNAL source 475 175 115 161 121 101 295 235 355 ATCAAGACCAACGTGGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCCGACATCCTTGCC 81 61 41 55 ArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProProProThr 160 IleLysArgAsnValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeuAla 120 GlyGluLysThrAlaGlyProAsnLeuAsnSerValArgGlyPheGluValIleAspThr 100 CGGCGGGACTCGACGACGGCGAGCGCGTCCCTTGCCAACAGCAACCTCCCGCAGTCGACG Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence An EST database from Sorghum: dark-grown seedlings Unpublished (2000) POLYA-No. Seq primer: JEN REV is 20. quality sequence stop: 95 /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
198 c 167 g 110 t Location/Qualifiers /organism="Sorghum bicolor" /db_xref="taxon:4558" 9.88e-72 793.00 94.198 90.128 49.448 Conservative: Mismatches: Indels: Gaps: Length: Matches: 566 570 155 7 10 0 294. 234 354 414 174

> Search completed: May 3, 2003, 13:15:25 Job time: 1089 secs